

SEQUENCE LISTING

<110> Microscience Limited

<120> VIRULENCE GENES AND PROTEINS, AND THEIR USE

<130> REP05921WO

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<170> PatentIn Ver. 2.1

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<210> 6

<211> 128

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1)..(126)

<400> 6

atg aaa ggt cgc ctg tta gat gct gtc ccg ctc agt tcc cta acg ggc 48
Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly
1 5 10 15

gtt ggc gca gcg ctt agt aac aag ctg gcg aaa atc aac ctg cat acc 96
Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr
20 25 30

gta cag gat tta ctc tta cac ctt cct ctg cg 128

Val Gln Asp Leu Leu Leu His Leu Pro Leu
35 40

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<211> 42

<212> PRT

<213> Escherichia coli

<400> 7

Met Lys Gly Arg Leu Leu Asp Ala Val Pro Leu Ser Ser Leu Thr Gly
1 5 10 15

Val Gly Ala Ala Leu Ser Asn Lys Leu Ala Lys Ile Asn Leu His Thr
20 25 30

Val Gln Asp Leu Leu Leu His Leu Pro Leu
35 40

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<211> 1174

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<213> Escherichia coli

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<222> (121)..(837)

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cactttgtta tcaatctggg gccagcaaat gctggcctga tttgttcttg aggggaagact 120

atg atg cgc aaa atg ctg ctg gcg gca gca ctt tca gtg acg gca atg 168
Met Met Arg Lys Met Leu Leu Ala Ala Ala Leu Ser Val Thr Ala Met
1 5 10 15

acc gct cac gcc gac tac cag tgc agc gtc acg ccg cgt gac gat gtg 216
Thr Ala His Ala Asp Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val
20 25 30

att gtc agc ccg caa acc gtg cag gtg aag ggc gaa aac ggc aat ctg 264
Ile Val Ser Pro Gln Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu
35 40 45

gtg atc acg cca gac ggc aac gtg atg tat aac ggt aag caa tat tcc 312

Val Ile Thr Pro Asp Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser
 50 55 60

ctg aat gcc gcc cag cgc gag cag gcg aag gat tat cag gct gaa cta 360
 Leu Asn Ala Ala Gln Arg Glu Gln Ala Lys Asp Tyr Gln Ala Glu Leu
 65 70 75 80

cgt agc acc ctg ccg tgg att gat gga ggc gcg aaa agc cgc gtc gag 408
 Arg Ser Thr Leu Pro Trp Ile Asp Gly Gly Ala Lys Ser Arg Val Glu
 85 90 95

aaa gct cgt att gcg ctg gat aaa att atc gtt cag gag atg ggc gaa 456
 Lys Ala Arg Ile Ala Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu
 100 105 110

agc agc aaa atg cgc agc cgt ctg acc aaa ctt gat gcg cag ctg aaa 504
 Ser Ser Lys Met Arg Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys
 115 120 125

gag cag atg aac cgc att atc gaa acg cgc agc gat ggc ctg acg ttt 552
 Glu Gln Met Asn Arg Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe
 130 135 140

cac tat aaa gcc att gat cag gtt cgt gcc gaa ggc cag caa tta gtg 600
 His Tyr Lys Ala Ile Asp Gln Val Arg Ala Glu Gly Gln Gln Leu Val
 145 150 155 160

aat cag gca atg ggc gga att tta cag gac agc att aat gaa atg ggc 648
 Asn Gln Ala Met Gly Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly
 165 170 175

gcg aaa gcg gtg ctg aaa agc ggc ggt aac cca tta cag aac gtg ctg 696
 Ala Lys Ala Val Leu Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu
 180 185 190

gga agc ctg ggc ggc ctg caa tcc tca atc caa acc gag tgg aaa aag 744
 Gly Ser Leu Gly Gly Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys
 195 200 205

cag gaa aaa gat ttc cag cag ttt ggc aaa gat gtt tgt agc cgc gtt 792
 Gln Glu Lys Asp Phe Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val
 210 215 220

gtg act ctg gaa gat agc cgc aaa gcc ctg gtc ggg aat tta aaa 837
 Val Thr Leu Glu Asp Ser Arg Lys Ala Leu Val Gly Asn Leu Lys
 225 230 235

taatcctcta tttaagacg gcataatact tttttatgcc gtttaattct tcgttttggt 897

acctgcctct aactttgtaa gggcgaattc tgcagatata catcacactg gcggccgctc 957
gagcatgcat ctagagggcc caattcgccc tatagtgagt cgtattacaa ttcactggcc 1017
gtcgttttac aaccgtcgtg actgggaaaa ccctggcggt acccaactta atcgccctgc 1077
agcacatccc cctttcgcca gctggcgtaa tagcgaaaag gcccgaccg atcgcccttc 1137
caacagttgc gcacctgatg gccaatggac ggcgctg 1174

<210> 9

<211> 239

<212> PRT

<213> Escherichia coli

<400> 9

Met Met Arg Lys Met Leu Leu Ala Ala Ala Leu Ser Val Thr Ala Met
1 5 10 15

Thr Ala His Ala Asp Tyr Gln Cys Ser Val Thr Pro Arg Asp Asp Val
20 25 30

Ile Val Ser Pro Gln Thr Val Gln Val Lys Gly Glu Asn Gly Asn Leu
35 40 45

Val Ile Thr Pro Asp Gly Asn Val Met Tyr Asn Gly Lys Gln Tyr Ser
50 55 60

Leu Asn Ala Ala Gln Arg Glu Gln Ala Lys Asp Tyr Gln Ala Glu Leu
65 70 75 80

Arg Ser Thr Leu Pro Trp Ile Asp Gly Gly Ala Lys Ser Arg Val Glu
85 90 95

Lys Ala Arg Ile Ala Leu Asp Lys Ile Ile Val Gln Glu Met Gly Glu
100 105 110

Ser Ser Lys Met Arg Ser Arg Leu Thr Lys Leu Asp Ala Gln Leu Lys
115 120 125

Glu Gln Met Asn Arg Ile Ile Glu Thr Arg Ser Asp Gly Leu Thr Phe
130 135 140

His Tyr Lys Ala Ile Asp Gln Val Arg Ala Glu Gly Gln Gln Leu Val
145 150 155 160

Asn Gln Ala Met Gly Gly Ile Leu Gln Asp Ser Ile Asn Glu Met Gly
 165 170 175

Ala Lys Ala Val Leu Lys Ser Gly Gly Asn Pro Leu Gln Asn Val Leu
 180 185 190

Gly Ser Leu Gly Gly Leu Gln Ser Ser Ile Gln Thr Glu Trp Lys Lys
 195 200 205

Gln Glu Lys Asp Phe Gln Gln Phe Gly Lys Asp Val Cys Ser Arg Val
 210 215 220

Val Thr Leu Glu Asp Ser Arg Lys Ala Leu Val Gly Asn Leu Lys
 225 230 235

<210> 10

<211> 3406

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (1007)..(1276)

<220>

<221> CDS

<222> (1280)..(1792)

<220>

<221> CDS

<222> (1798)..(2574)

<220>

<221> CDS

<222> (2604)..(3398)

<400> 10

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ctttcgcgac agctttttcc atgctgatat gcaccctggc aacatcttcg taagctatga 180

acacccggaa aacccgaaat atatcgcat tgattgcggg attgttggt cgctaaacaa 240

agaagataaa cgctatctgg cggaaaactt tatgccttc ttaaatcgcg actatcgcaa 300

18

His Asp Lys Glu Gln Val	Val Phe Asp Ile Gly Phe Ser Glu	
85	90	95
ctg cta ttg gtg ttc atc atc ggc ctc gtc gtt ctg ggg ccg caa cga		1351
Leu Leu Leu Val Phe Ile Ile Gly Leu Val Val Leu Gly Pro Gln Arg		
100	105	110
ctg cct gtg gcg gta aaa acg gta gcg ggc tgg att cgc gcg ttg cgt		1399
Leu Pro Val Ala Val Lys Thr Val Ala Gly Trp Ile Arg Ala Leu Arg		
115	120	125 130
tca ctg gcg aca acg gtg cag aac gaa ctg acc cag gag tta aaa ctc		1447
Ser Leu Ala Thr Thr Val Gln Asn Glu Leu Thr Gln Glu Leu Lys Leu		
	135	140 145
cag gag ttt cag gac agt ctg aaa aag gtt gaa aag gcg agc ctc act		1495
Gln Glu Phe Gln Asp Ser Leu Lys Lys Val Glu Lys Ala Ser Leu Thr		
	150	155 160
aac ctg acg ccc gaa ctg aaa gcg tcg atg gat gaa tta cgc cag gct		1543
Asn Leu Thr Pro Glu Leu Lys Ala Ser Met Asp Glu Leu Arg Gln Ala		
	165	170 175
gcg gag tcg atg aaa cgt tcc tac gtt gca aac gat cct gaa aag gcg		1591
Ala Glu Ser Met Lys Arg Ser Tyr Val Ala Asn Asp Pro Glu Lys Ala		
	180	185 190
agc gat gaa gcg cac acc atc cat aac ccg gtg gtg aaa gac aat gaa		1639
Ser Asp Glu Ala His Thr Ile His Asn Pro Val Val Lys Asp Asn Glu		
	195	200 205 210
act gcg cat gaa ggc gta acg cct gct gct gca caa acg cag gcc agt		1687
Thr Ala His Glu Gly Val Thr Pro Ala Ala Ala Gln Thr Gln Ala Ser		
	215	220 225
tcg ccg gaa cag aag cca gaa acc acg cca gag ccg gtg gta aaa cct		1735
Ser Pro Glu Gln Lys Pro Glu Thr Thr Pro Glu Pro Val Val Lys Pro		
	230	235 240
gct gcg gac gct gaa ccg aaa acc gct gca cct tcc cct tcg tcg agt		1783
Ala Ala Asp Ala Glu Pro Lys Thr Ala Ala Pro Ser Pro Ser Ser Ser		
	245	250 255
gat aaa ccg taaac atg tct gta gaa gat act caa ccg ctt atc acg cat		1833
Asp Lys Pro Met Ser Val Glu Asp Thr Gln Pro Leu Ile Thr His		
	260	265 270
ctg att gag ctg cgt aag cgt ctg ctg aac tgc att atc tcg gtg atc		1881

Leu Ile Glu Leu Arg Lys Arg Leu Leu Asn Cys Ile Ile Ser Val Ile
 275 280 285

gtg ata ttc ctg tgt ctg gtc tat ttc gcc aat gac atc tat cac ctg 1929
 Val Ile Phe Leu Cys Leu Val Tyr Phe Ala Asn Asp Ile Tyr His Leu
 290 295 300 305

gta tcc gcg cca ctg atc aag cag ttg ccg caa ggt tca acg atg atc 1977
 Val Ser Ala Pro Leu Ile Lys Gln Leu Pro Gln Gly Ser Thr Met Ile
 310 315 320

gcc acc gac gtg gcc tcg ccg ttc ttt acg ccg atc aag ctg acc ttt 2025
 Ala Thr Asp Val Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe
 325 330 335

atg gtg tcg ctg att ctg tca gcg ccg gtg att ctc tat cag gtg tgg 2073
 Met Val Ser Leu Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp
 340 345 350

gcg ttt atc gcc cca gcg ctg tat aag cat gaa cgt cgc ctg gtg gtg 2121
 Ala Phe Ile Ala Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val
 355 360 365

ccg ctg ctg gtt tcc agc tct ctg ctg ttt tat atc ggc atg gcg ttc 2169
 Pro Leu Leu Val Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe
 370 375 380 385

gcc tac ttt gtg gtc ttt ccg ctg gca ttt ggc ttc ctt gcc aat acc 2217
 Ala Tyr Phe Val Val Phe Pro Leu Ala Phe Gly Phe Leu Ala Asn Thr
 390 395 400

gcg ccg gaa ggg gta cag gta tcc acc gac atc gcg agc tat tta agc 2265
 Ala Pro Glu Gly Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser
 405 410 415

ttc gtt atg gcg ctg ttt atg gcg ttt ggt gtc tcc ttt gaa gtg ccg 2313
 Phe Val Met Ala Leu Phe Met Ala Phe Gly Val Ser Phe Glu Val Pro
 420 425 430

gtg gca att gtg ctg ctg tgc tgg atg ggg att acc tcg cca gaa gac 2361
 Val Ala Ile Val Leu Leu Cys Trp Met Gly Ile Thr Ser Pro Glu Asp
 435 440 445

tta cgc aaa aaa cgc ccg tat gtg ctg gtt ggt gca ttc gtt gtc ggg 2409
 Leu Arg Lys Lys Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly
 450 455 460 465

atg ttg ctg acg ccg ccg gat gtc ttc tcg caa acg ctg ttg gcg atc 2457

Met	Leu	Leu	Thr	Pro	Pro	Asp	Val	Phe	Ser	Gln	Thr	Leu	Leu	Ala	Ile	
				470					475					480		
cct	atg	tac	tgc	ctg	ttt	gaa	atc	ggg	gtc	ttc	ttc	tca	cgc	ttt	tac	2505
Pro	Met	Tyr	Cys	Leu	Phe	Glu	Ile	Gly	Val	Phe	Phe	Ser	Arg	Phe	Tyr	
			485					490					495			
gtt	ggg	aaa	ggg	cga	aac	cgg	gaa	gag	gaa	aac	gac	gct	gaa	gca	gaa	2553
Val	Gly	Lys	Gly	Arg	Asn	Arg	Glu	Glu	Glu	Asn	Asp	Ala	Glu	Ala	Glu	
		500					505				510					
agc	gaa	aaa	act	gaa	gaa	taa	attcaaccgc	ccgtcagggc	ggttgtcat	atg						2606
Ser	Glu	Lys	Thr	Glu	Glu					Met						
		515				520										
gag	tac	agg	atg	ttt	gat	atc	ggc	gtt	aat	ttg	acc	agt	tcg	caa	ttt	2654
Glu	Tyr	Arg	Met	Phe	Asp	Ile	Gly	Val	Asn	Leu	Thr	Ser	Ser	Gln	Phe	
			525					530					535			
gcg	aaa	gac	cgt	gat	gat	gtt	gta	gcg	cgc	gct	ttt	gac	gcg	gga	gtt	2702
Ala	Lys	Asp	Arg	Asp	Asp	Val	Val	Ala	Arg	Ala	Phe	Asp	Ala	Gly	Val	
		540					545					550				
aat	ggg	cta	ctc	atc	acc	ggg	acc	aat	ctg	cgt	gaa	agc	cag	cag	gcg	2750
Asn	Gly	Leu	Leu	Ile	Thr	Gly	Thr	Asn	Leu	Arg	Glu	Ser	Gln	Gln	Ala	
		555				560					565					
caa	aag	ctg	gcg	cgt	cag	tat	tcg	tcc	tgt	tgg	tca	acg	gcg	ggc	gta	2798
Gln	Lys	Leu	Ala	Arg	Gln	Tyr	Ser	Ser	Cys	Trp	Ser	Thr	Ala	Gly	Val	
		570			575				580					585		
cat	cct	cac	gac	agc	agc	cag	tgg	caa	gct	gtg	act	gaa	gaa	gcg	att	2846
His	Pro	His	Asp	Ser	Ser	Gln	Trp	Gln	Ala	Val	Thr	Glu	Glu	Ala	Ile	
			590						595					600		
att	gag	ctg	gcc	gcg	cag	cca	gaa	gtg	gtg	gcg	att	ggg	gaa	tgt	ggg	2894
Ile	Glu	Leu	Ala	Ala	Gln	Pro	Glu	Val	Val	Ala	Ile	Gly	Glu	Cys	Gly	
			605					610					615			
ctc	gac	ttt	aac	cgc	aac	ttt	tcg	acg	ccg	gaa	gag	cag	gaa	cgc	gct	2942
Leu	Asp	Phe	Asn	Arg	Asn	Phe	Ser	Thr	Pro	Glu	Glu	Gln	Glu	Arg	Ala	
			620					625					630			
ttt	gtt	gcc	cag	cta	cgc	att	gcc	gca	gaa	tta	aac	atg	ccg	gta	ttt	2990
Phe	Val	Ala	Gln	Leu	Arg	Ile	Ala	Ala	Glu	Leu	Asn	Met	Pro	Val	Phe	
		635				640					645					
atg	cac	tgt	cgc	gat	gcc	cac	gag	cgg	ttt	atg	aca	ttg	ctg	gag	ccg	3038

Met His Cys Arg Asp Ala His Glu Arg Phe Met Thr Leu Leu Glu Pro
650 655 660 665

tgg ctg gat aaa ctg cct ggt gcg gtt ctt cat tgc ttt acc ggc aca 3086
Trp Leu Asp Lys Leu Pro Gly Ala Val Leu His Cys Phe Thr Gly Thr
670 675 680

cgc gaa gag atg cag gcg tgc gtg gcg tgt gga att tat atc ggc att 3134
Arg Glu Glu Met Gln Ala Cys Val Ala Cys Gly Ile Tyr Ile Gly Ile
685 690 695

acc ggt tgg gtt tgc gat gaa cga cgc ggg ctg gag ctg cgg gaa ttg 3182
Thr Gly Trp Val Cys Asp Glu Arg Arg Gly Leu Glu Leu Arg Glu Leu
700 705 710

ttg ccg ttg att ccg gcg gag aaa ttg ctg atc gaa act gat gcg ccg 3230
Leu Pro Leu Ile Pro Ala Glu Lys Leu Leu Ile Glu Thr Asp Ala Pro
715 720 725

tat ctg ctc cct cgc gat ctc acg cca aag cca tca tcc cgg cgc aac 3278
Tyr Leu Leu Pro Arg Asp Leu Thr Pro Lys Pro Ser Ser Arg Arg Asn
730 735 740 745

gag cca gcc cat ctg ccc cat att ttg caa cgt att gcg cac tgg cgt 3326
Glu Pro Ala His Leu Pro His Ile Leu Gln Arg Ile Ala His Trp Arg
750 755 760

gga gaa gat gcc gca tgg ctg gct gcc acc acg gat gcc aat gtc aaa 3374
Gly Glu Asp Ala Ala Trp Leu Ala Ala Thr Thr Asp Ala Asn Val Lys
765 770 775

aca ctg ttt ggg att gcg ttt tag agtttgcg 3406
Thr Leu Phe Gly Ile Ala Phe
780 785

<210> 11

<211> 89

<212> PRT

<213> Escherichia coli

<400> 11

Met Gly Gly Ile Ser Ile Trp Gln Leu Leu Ile Ile Ala Val Ile Val
1 5 10 15

Val Leu Leu Phe Gly Thr Lys Lys Leu Gly Ser Ile Gly Ser Asp Leu
20 25 30

Gly Ala Ser Ile Lys Gly Phe Lys Lys Ala Met Ser Asp Asp Glu Pro
 35 40 45

Lys Gln Asp Lys Thr Ser Gln Asp Ala Asp Phe Thr Ala Lys Thr Ile
 50 55 60

Ala Asp Lys Gln Ala Asp Thr Asn Gln Glu Gln Ala Lys Ile Glu Asp
 65 70 75 80

Ala Lys Arg His Asp Lys Glu Gln Val
 85

<210> 12

<211> 171

<212> PRT

<213> Escherichia coli

<400> 12

Val Phe Asp Ile Gly Phe Ser Glu Leu Leu Leu Val Phe Ile Ile Gly
 1 5 10 15

Leu Val Val Leu Gly Pro Gln Arg Leu Pro Val Ala Val Lys Thr Val
 20 25 30

Ala Gly Trp Ile Arg Ala Leu Arg Ser Leu Ala Thr Thr Val Gln Asn
 35 40 45

Glu Leu Thr Gln Glu Leu Lys Leu Gln Glu Phe Gln Asp Ser Leu Lys
 50 55 60

Lys Val Glu Lys Ala Ser Leu Thr Asn Leu Thr Pro Glu Leu Lys Ala
 65 70 75 80

Ser Met Asp Glu Leu Arg Gln Ala Ala Glu Ser Met Lys Arg Ser Tyr
 85 90 95

Val Ala Asn Asp Pro Glu Lys Ala Ser Asp Glu Ala His Thr Ile His
 100 105 110

Asn Pro Val Val Lys Asp Asn Glu Thr Ala His Glu Gly Val Thr Pro
 115 120 125

Ala Ala Ala Gln Thr Gln Ala Ser Ser Pro Glu Gln Lys Pro Glu Thr
 130 135 140

Thr Pro Glu Pro Val Val Lys Pr Ala Ala Asp Ala Glu Pr Lys Thr
 145 150 155 160

Ala Ala Pro Ser Pro Ser Ser Ser Asp Lys Pro
 165 170

<210> 13

<211> 258

<212> PRT

<213> Escherichia coli

<400> 13

Met Ser Val Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu
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Arg Lys Arg Leu Leu Asn Cys Ile Ile Ser Val Ile Val Ile Phe Leu
 20 25 30

Cys Leu Val Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ser Ala Pro
 35 40 45

Leu Ile Lys Gln Leu Pro Gln Gly Ser Thr Met Ile Ala Thr Asp Val
 50 55 60

Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu
 65 70 75 80

Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala
 85 90 95

Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val
 100 105 110

Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val
 115 120 125

Val Phe Pro Leu Ala Phe Gly Phe Leu Ala Asn Thr Ala Pro Glu Gly
 130 135 140

Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala
 145 150 155 160

Leu Phe Met Ala Phe Gly Val Ser Phe Glu Val Pro Val Ala Ile Val
 165 170 175

Leu Leu Cys Trp Met Gly Ile Thr Ser Pro Glu Asp Leu Arg Lys Lys
 180 185 190

Arg Pro Tyr Val Leu Val Gly Ala Phe Val Val Gly Met Leu Leu Thr

195	200	205
Pro Pro Asp Val Phe Ser Gln Thr Leu Leu Ala Ile Pro Met Tyr Cys		
210	215	220
Leu Phe Glu Ile Gly Val Phe Phe Ser Arg Phe Tyr Val Gly Lys Gly		
225	230	235 240
Arg Asn Arg Glu Glu Glu Asn Asp Ala Glu Ala Glu Ser Glu Lys Thr		
245	250	255

Glu Glu

<210> 14

<211> 264

<212> PRT

<213> Escherichia coli

<400> 14

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1 5 10 15

Phe Ala Lys Asp Arg Asp Asp Val Val Ala Arg Ala Phe Asp Ala Gly
20 25 30

Val Asn Gly Leu Leu Ile Thr Gly Thr Asn Leu Arg Glu Ser Gln Gln
35 40 45

Ala Gln Lys Leu Ala Arg Gln Tyr Ser Ser Cys Trp Ser Thr Ala Gly
50 55 60

Val His Pro His Asp Ser Ser Gln Trp Gln Ala Val Thr Glu Glu Ala
65 70 75 80

Ile Ile Glu Leu Ala Ala Gln Pro Glu Val Val Ala Ile Gly Glu Cys
85 90 95

Gly Leu Asp Phe Asn Arg Asn Phe Ser Thr Pro Glu Glu Gln Glu Arg
100 105 110

Ala Phe Val Ala Gln Leu Arg Ile Ala Ala Glu Leu Asn Met Pro Val
115 120 125

Phe Met His Cys Arg Asp Ala His Glu Arg Phe Met Thr Leu Leu Glu
130 135 140

Pro Trp Leu Asp Lys Leu Pro Gly Ala Val Leu His Cys Phe Thr Gly

ttt ggg act aag aag tta cgt acg ctg ggc qga qac ctt gga gcg gcc 274

Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu Gly Ala Ala
 20 25 30 35

att aaa ggg ttc aag aag gcg atg aat gat gac gat gct gcg gcg aaa 322
 Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala Ala Ala Lys
 40 45 50

aaa ggc gca gac gtt gat ctt cag gct gaa aag ctc tct cat aaa gag 370
 Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser His Lys Glu
 55 60 65

tgacgtggcg agcaggacgc tccctcaata tcttgttcga tacaaaaacc cgcttcaaaa 430

agcggggtttt ttatcagaca gatgtaagta attattacag gattacttaa cttccatccc 490

tttcgcctgc aaatcggcgt ggtaagaaga gcggacaaac ggaccgcatg cagcatgggt 550

aaagcccatc gccagcgctt cgctttcatt tcgtcg 586

<210> 16

<211> 67

<212> PRT

<213> Escherichia coli

<400> 16

Met Gly Glu Ile Ser Ile Thr Lys Leu Leu Val Val Ala Ala Leu Val
 1 5 10 15

Val Leu Leu Phe Gly Thr Lys Lys Leu Arg Thr Leu Gly Gly Asp Leu
 20 25 30

Gly Ala Ala Ile Lys Gly Phe Lys Lys Ala Met Asn Asp Asp Asp Ala
 35 40 45

Ala Ala Lys Lys Gly Ala Asp Val Asp Leu Gln Ala Glu Lys Leu Ser
 50 55 60

His Lys Glu
 65

<210> 17

<211> 4200

<212> DNA

<213> Salmonella typhimurium

<220>

<221> CDS

<222> (947)..(1444)

<220>

<221> CDS

<222> (1450)..(1722)

<400> 17

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ctaacaaaga ggcagcgtga aggataatgt gtataatgcg gccctaataa ttcacatcatct 120

atcacagagg aacatgtatg ggtgggtatca gtatttggca gttgttgatt gttgccgtta 180

tcgtcgtact gctgttcggc accaaaaaac tcggttccat cggttccgat cttggcgcgt 240

ctatcaaagg ctttaaaaag gccatgagcg atgatgatgc caaacaggat aaaaccagtc 300

aggacgctga ttttaccgct aaatctatcg cggataagca aggccaagcg aaaaaggaag 360

acgctaaaag ccaagataaa gagcagggtat aatccgtgtt tgatatcggg tttagcgaac 420

tgctgttagt gttcgttata ggccctcattg tgttggggcc gcaacgattg ccagtagcgg 480

taaaaacggg agcgggctgg attcgcgcgt tgcggtccct tgcgacaacg gttcagaatg 540

aactgactca ggaactgaaa cttcaggagt tccaggacag tctgaaaaaa gtcgaaaagg 600

cgagcctgga aaatctgact cccgaactga aagcatctat ggatgaactg cgtcaggcgg 660

cggagtcgat gaaacgcacc tacagcgcta acgatcccga acaagcgagc gatgaagcgc 720

ataccatcca taatccggtg gtaaaaggga acgaaacgca gcatgagggc gtcacccttg 780

ccgccgctga aacacaggcg agcgcgccgg aacaaaagcc ggagcccgtt aaagctaacg 840

tgccctgagtc gacggaaacc gcttccgtag ccacgataga cgccgagaag aaatccgctg 900

cgccctgttgt cgaatcttcc cctcgtcga gtgataaacc gtaaac atg gct gta 955

Met Ala Val

1

gaa gat act caa ccg ctt atc acg cat ctg atc gag ttg cgt aag cgc 1003

Glu Asp Thr Gln Pro Leu Ile Thr His Leu Ile Glu Leu Arg Lys Arg

5

10

15

ctg cta aac tgc atc gtc gca gta ctt ctg att ttt ctg gcg tta att 1051

Leu Leu Asn Cys Ile Val Ala Val Leu Leu Ile Phe Leu Ala Leu Ile
 20 25 30 35

 tat ttc gcc aat gat att tat cat tta gtc gcc gca ccg ctg att aaa 1099
 Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro Leu Ile Lys
 40 45 50

 cag atg ccg caa ggg gcg aca atg att gcg acg gat gtg gcg tcg ccg 1147
 Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val Ala Ser Pro
 55 60 65

 ttt ttt acg cct atc aaa ctc acc ttc atg gtg tct ttg atc tta tcc 1195
 Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu Ile Leu Ser
 70 75 80

 gcg cct gtc att ttg tac cag gtt tgg gcc ttt atc gcc ccg gcg ctg 1243
 Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala Pro Ala Leu
 85 90 95

 tat aag cat gag cgt cgt ctg gtc gta cct ctg ctg gta tcc agc tcg 1291
 Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val Ser Ser Ser
 100 105 110 115

 ctg ctt ttc tat att ggt atg gcc ttc gcc tat ttt gtc gta ttc cct 1339
 Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val Val Phe Pro
 120 125 130

 ttg gcc ttt ggt ttc ctg acg cat acg gcg ccg gaa ggg gta cag gtt 1387
 Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly Val Gln Val
 135 140 145

 tcg aca gat atc gcc agc tat ctt agc ttt gtc atg gcg ctt ttt atg 1435
 Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala Leu Phe Met
 150 155 160

 gcc ttt gcg tagcc ttt gaa gtg ccg gtg gcg att gtg ttg ctg tgc tgg 1485
 Ala Phe Ala Phe Glu Val Pro Val Ala Ile Val Leu Leu Cys Trp
 165 170 175

 atg ggc atc acc acg cca gaa gat ttg cgt aaa aaa cgg cct tat atc 1533
 Met Gly Ile Thr Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile
 180 185 190

 ctg gtc ggg gca ttc att gtg gga atg ctg ctt acg ccg cca gat gtt 1581
 Leu Val Gly Ala Phe Ile Val Gly Met Leu Leu Thr Pro Pro Asp Val
 195 200 205 210

 ttc tcg caa acg ttg ctg gcg ata ccg atg tac tgc ctg ttt gaa att 1629

Phe Ser Gln Thr Leu Leu Ala Ile Pro Met Tyr Cys Leu Phe Glu Ile
 215 220 225

ggc gtt ttc tgc tca cgc ttt tat gtc ggt aag cga cgg acg cgc gac 1677
 Gly Val Phe Cys Ser Arg Phe Tyr Val Gly Lys Arg Arg Thr Arg Asp
 230 235 240

gaa gat aac gag gcc gaa acc gaa aag gcc gag cac act gaa gac 1722
 Glu Asp Asn Glu Ala Glu Thr Glu Lys Ala Glu His Thr Glu Asp
 245 250 255

taaacacaac cgccccccag ggcggttgtc atatgggggc aagcatgttt gatattggcg 1782

ttaatttaac cagtagccag ttgcaaaag atcgtgatga tgtggtcgcc cgtgcgtttg 1842

cggcgggagt aaaaggtatg ctactgaccg gaacgaacat ccatgaaagt cagcaggcgt 1902

taaaactggc gcggcgctac cccattgtt ggtcgacggc tggcgtccat cccatgaca 1962

gcagtcagt gtcaccgcg tctgaagacg ccattattgc gctggcgaac cagccggaag 2022

tcgtcgctat cggtagtg gggctggatt tcaatcgcaa ttttccacg ccgcaggagc 2082

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 <212> PRT
 <213> Salmonella typhimurium

<400> 18
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 Arg Lys Arg Leu Leu Asn Cys Ile Val Ala Val Leu Leu Ile Phe Leu
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 Ala Leu Ile Tyr Phe Ala Asn Asp Ile Tyr His Leu Val Ala Ala Pro
 35 40 45
 Leu Ile Lys Gln Met Pro Gln Gly Ala Thr Met Ile Ala Thr Asp Val
 50 55 60
 Ala Ser Pro Phe Phe Thr Pro Ile Lys Leu Thr Phe Met Val Ser Leu
 65 70 75 80
 Ile Leu Ser Ala Pro Val Ile Leu Tyr Gln Val Trp Ala Phe Ile Ala
 85 90 95
 Pro Ala Leu Tyr Lys His Glu Arg Arg Leu Val Val Pro Leu Leu Val
 100 105 110
 Ser Ser Ser Leu Leu Phe Tyr Ile Gly Met Ala Phe Ala Tyr Phe Val
 115 120 125
 Val Phe Pro Leu Ala Phe Gly Phe Leu Thr His Thr Ala Pro Glu Gly
 130 135 140
 Val Gln Val Ser Thr Asp Ile Ala Ser Tyr Leu Ser Phe Val Met Ala
 145 150 155 160
 Leu Phe Met Ala Phe Ala
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<210> 19
 <211> 91
 <212> PRT
 <213> Salmonella typhimurium

<400> 19
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Thr Pro Glu Asp Leu Arg Lys Lys Arg Pro Tyr Ile Leu Val Gly Ala
20 25 30

Phe Ile Val Gly Met Leu Leu Thr Pro Pro Asp Val Phe Ser Gln Thr
35 40 45

Leu Leu Ala Ile Pro Met Tyr Cys Leu Phe Glu Ile Gly Val Phe Cys
50 55 60

Ser Arg Phe Tyr Val Gly Lys Arg Arg Thr Arg Asp Glu Asp Asn Glu
65 70 75 80

Ala Glu Thr Glu Lys Ala Glu His Thr Glu Asp
85 90

<210> 20

<211> 2601

<212> DNA

<213> Neisseria meningitidis

<220>

<221> CDS

<222> (1572)..(2339)

<400> 20

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caaaaacccg tcccacctgg ttacgaagt tgccgactta tggtttcaca ccatgattct 120

tctgacacac caccgacctga aggcggaaga cgtattggac gaacttgccg gccgccaagg 180

tttgctgggc ttggccgaaa aagccgctcg cacagaatct tgaatttata ttaaaatccg 240

cactttccca cattcaatcc gtctgaccgc tggtcagacg gcatcggagc cgttatggac 300

aactgtatatt tctgcaaaat cgccgcaaaa gacattccgg cgcaaaccgt ctatgaagac 360

ggcgaaatgg tttgtttcaa agacatcaac cccgctgctc cggttcatct gctgctgatt 420

cccaaagtcc atttcgattc gttggcacac gccgcgcccc aacatcagcc ccttttgagg 480

aaaatgatgc tgaaagttcc cgaaatcgcc aaagcggcag gactggcaga cggcttcaaa 540

accctgatca acaccggaaa aggcggcgga caagaggtct tccacctgca tatacacatc 600

atgggcacac ccgtataaac cggtatttca caatcaaccc ctaatactta cttaaggata 660
 catcatgggc agttttttctc tgacgcactg gattatcgta ctgattatcg tcgttttgat 720
 attcggcacc aaaaaactgc gcaacgtcgg caaagacctc ggcggtgcgg ttcatgactt 780
 caaacagggg ctgaacgaag gtacagacgg caaagaagcc caaaaagacg atgtaatcga 840
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 Val Ser Glu Thr Gln Asn Glu Gln Pro Val Gln Pro Leu
 1 5 10
 gtc gag cat ctc atc gag ctg cgc cgc cgc ctg atg tgg acg gtt gtc 1658
 Val Glu His Leu Ile Glu Leu Arg Arg Arg Leu Met Trp Thr Val Val
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 ggt atc tta gtc tgc ttt ttc ggc cta atg ccg ttt gcc caa caa ctc 1706
 Gly Ile Leu Val Cys Phe Phe Gly Leu Met Pro Phe Ala Gln Gln Leu
 30 35 40 45
 tat act ttt atc gcc gac ccg ctg atg gca aac ctg ccc aaa gac acc 1754
 Tyr Thr Phe Ile Ala Asp Pro Leu Met Ala Asn Leu Pro Lys Asp Thr
 50 55 60

agc atg att gcc acc gat gtc atc gca cca ttt ttc gtg ccg gtc aaa 1802
 Ser Met Ile Ala Thr Asp Val Ile Ala Pro Phe Phe Val Pro Val Lys
 65 70 75

gtt acc ctg atg gcg gca ttt tta att tcg ctg ccg cat acg ctc tac 1850
 Val Thr Leu Met Ala Ala Phe Leu Ile Ser Leu Pro His Thr Leu Tyr
 80 85 90

caa atc tgg gca ttc gtc gcc ccc gca ctc tac caa aac gaa aaa cgc 1898
 Gln Ile Trp Ala Phe Val Ala Pro Ala Leu Tyr Gln Asn Glu Lys Arg
 95 100 105

ctg att acg ccg ctc gtc ctc tcc agc gtc agc ctg ttt ttc atc ggc 1946
 Leu Ile Thr Pro Leu Val Leu Ser Ser Val Ser Leu Phe Phe Ile Gly
 110 115 120 125

atg gca ttt gcc tac ttt ttg gtt ttc ccc gtc att ttc aaa ttc ctt 1994
 Met Ala Phe Ala Tyr Phe Leu Val Phe Pro Val Ile Phe Lys Phe Leu
 130 135 140

gcc agc gtt acc cct gtc ggt gtc aat atg gcg aca gac atc gac aaa 2042
 Ala Ser Val Thr Pro Val Gly Val Asn Met Ala Thr Asp Ile Asp Lys
 145 150 155

tac ctc tcc ttc atc ttg ggg atg ttt gtc gca ttc ggt aca acg ttt 2090
 Tyr Leu Ser Phe Ile Leu Gly Met Phe Val Ala Phe Gly Thr Thr Phe
 160 165 170

gaa gtc ccc att gtc gtt atc ctg tta acc aaa att ggt gtg gta aca 2138
 Glu Val Pro Ile Val Val Ile Leu Leu Thr Lys Ile Gly Val Val Thr
 175 180 185

acc gaa cag ctc aaa cgc gcc cgc ccc tat gtg att gtc ggc gcg ttt 2186
 Thr Glu Gln Leu Lys Arg Ala Arg Pro Tyr Val Ile Val Gly Ala Phe
 190 195 200 205

gtc att gcc gcc atc atc acg ccg ccc gat gtg att tca caa acc ctg 2234
 Val Ile Ala Ala Ile Ile Thr Pro Pro Asp Val Ile Ser Gln Thr Leu
 210 215 220

ctt gcc att ccg ctg att ctc tta tac gaa gca ggt att tgg ttc gga 2282
 Leu Ala Ile Pro Leu Ile Leu Leu Tyr Glu Ala Gly Ile Trp Phe Gly
 225 230 235

cgc ttt ttc acg cca cgt tca gaa cag gat ggc gac ata cag ccg cct 2330
 Arg Phe Phe Thr Pro Arg Ser Glu Gln Asp Gly Asp Ile Gln Pro Pro
 240 245 250

gca aca acc tgacactatg ccgtccgaac ctccgcctca taccgccaca 2379
 Ala Thr Thr
 255

gattaaggaa tacctttgaa taccctctat ttaggttcaa acagcccgcg ccgaatggaa 2439
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<210> 21

<211> 256

<212> PRT

<213> Neisseria meningitidis

<400> 21

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 20 25 30

Val Cys Phe Phe Gly Leu Met Pro Phe Ala Gln Gln Leu Tyr Thr Phe
 35 40 45

Ile Ala Asp Pro Leu Met Ala Asn Leu Pro Lys Asp Thr Ser Met Ile
 50 55 60

Ala Thr Asp Val Ile Ala Pro Phe Phe Val Pro Val Lys Val Thr Leu
 65 70 75 80

Met Ala Ala Phe Leu Ile Ser Leu Pro His Thr Leu Tyr Gln Ile Trp
 85 90 95

Ala Phe Val Ala Pro Ala Leu Tyr Gln Asn Glu Lys Arg Leu Ile Thr
 100 105 110

Pro Leu Val Leu Ser Ser Val Ser Leu Phe Phe Ile Gly Met Ala Phe
 115 120 125

Ala Tyr Phe Leu Val Phe Pr Val Ile Phe Lys Phe Leu Ala Ser Val
 130 135 140

Thr Pr Val Gly Val Asn Met Ala Thr Asp Ile Asp Lys Tyr Leu Ser
 145 150 155 160

Phe Ile Leu Gly Met Phe Val Ala Phe Gly Thr Thr Phe Glu Val Pro
 165 170 175

Ile Val Val Ile Leu Leu Thr Lys Ile Gly Val Val Thr Thr Glu Gln
 180 185 190

Leu Lys Arg Ala Arg Pro Tyr Val Ile Val Gly Ala Phe Val Ile Ala
 195 200 205

Ala Ile Ile Thr Pro Pro Asp Val Ile Ser Gln Thr Leu Leu Ala Ile
 210 215 220

Pro Leu Ile Leu Leu Tyr Glu Ala Gly Ile Trp Phe Gly Arg Phe Phe
 225 230 235 240

Thr Pro Arg Ser Glu Gln Asp Gly Asp Ile Gln Pro Pro Ala Thr Thr
 245 250 255

<210> 22

<211> 4604

<212> DNA

<213> Escherichia coli

<220>

<221> CDS

<222> (2982)..(4082)

<220>

<221> CDS

<222> (1534)..(2637)

<220>

<221> CDS

<222> (749)..(1531)

<220>

<221> CDS

<222> (6)..(746)

<400> 22

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tcg ctg ata aag tac agc gag aca gat tat aca att tat tgt gac caa 98

Ser	Leu	Ile	Lys	Tyr	Ser	Glu	Thr	Asp	Tyr	Thr	Ile	Tyr	Cys	Asp	Gln	
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Asp	Asp	Ile	Trp	Leu	Glu	Asn	Lys	Ile	Phe	Glu	Leu	Val	Lys	Tyr	Ala	
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aat	gaa	att	aaa	ttg	aat	gta	tca	gat	gcg	cct	tcg	cta	ggt	tat	gct	194
Asn	Glu	Ile	Lys	Leu	Asn	Val	Ser	Asp	Ala	Pro	Ser	Leu	Val	Tyr	Ala	
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gat	ggc	tat	gct	tat	atg	gat	ggg	gag	ggg	aca	atc	gat	ttt	tct	ggg	242
Asp	Gly	Tyr	Ala	Tyr	Met	Asp	Gly	Glu	Gly	Thr	Ile	Asp	Phe	Ser	Gly	
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Ile	Ser	Asn	Asn	His	Ala	Asp	Gln	Leu	Lys	Asp	Phe	Leu	Phe	Phe	Asn	
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Gly	Gly	Tyr	Gln	Gly	Cys	Ser	Ile	Met	Phe	Asn	Arg	Ala	Met	Thr	Lys	
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Phe	Leu	Leu	Asn	Tyr	Arg	Gly	Phe	Val	Tyr	Leu	His	Asp	Asp	Ile	Thr	
			115					120					125			
aca	tta	gct	gca	tac	gct	ctt	ggg	aaa	gtt	tat	ttt	ctc	ccg	aaa	tac	434
Thr	Leu	Ala	Ala	Tyr	Ala	Leu	Gly	Lys	Val	Tyr	Phe	Leu	Pro	Lys	Tyr	
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Leu	Met	Leu	Tyr	Arg	Gln	His	Thr	Asn	Ala	Val	Thr	Gly	Ile	Lys	Thr	
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ttc	cgc	aat	gga	ttg	act	tct	aaa	ttt	aaa	tca	cca	gta	aac	tat	ctt	530
Phe	Arg	Asn	Gly	Leu	Thr	Ser	Lys	Phe	Lys	Ser	Pro	Val	Asn	Tyr	Leu	
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Leu	Ser	Arg	Lys	His	Tyr	Gln	Val	Lys	Lys	Ser	Phe	Phe	Glu	Cys	Asn	
				180					185					190		
agc	tct	atc	tta	tca	gag	acg	aat	aaa	aaa	gtt	ttt	ttg	gat	ttt	att	626
Ser	Ser	Ile	Leu	Ser	Glu	Thr	Asn	Lys	Lys	Val	Phe	Leu	Asp	Phe	Ile	
			195					200					205			
tca	ttt	tgt	gaa	tca	aat	aat	aaa	ttt	aca	gat	ttt	ttt	aag	tta	tgg	674

Ser	Phe	Cys	Glu	Ser	Asn	Asn	Lys	Phe	Thr	Asp	Phe	Phe	Lys	Leu	Trp	
		210					215						220			
cga	ggg	ggg	ttt	aga	tta	aat	aac	agt	aga	act	aaa	tta	tta	tta	aaa	722
Arg	Gly	Gly	Phe	Arg	Leu	Asn	Asn	Ser	Arg	Thr	Lys	Leu	Leu	Leu	Lys	
		225				230					235					
ttc	tta	ata	cgg	aga	aaa	ttt	agc	ga	atg	att	tca	ata	ctt	aca	cct	769
Phe	Leu	Ile	Arg	Arg	Lys	Phe	Ser		Met	Ile	Ser	Ile	Leu	Thr	Pro	
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Thr	Phe	Asn	Arg	Gln	His	Thr	Leu	Ser	Arg	Leu	Phe	Asn	Ser	Leu	Ile	
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Leu	Gln	Thr	Asp	Lys	Asp	Phe	Glu	Trp	Ile	Ile	Ile	Asp	Asp	Gly	Ser	
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ata	gat	gca	aca	gcg	gta	ctt	gta	gaa	gat	ttt	aga	aaa	aaa	tgt	gat	913
Ile	Asp	Ala	Thr	Ala	Val	Leu	Val	Glu	Asp	Phe	Arg	Lys	Lys	Cys	Asp	
			290					295						300		
ttt	gac	ttg	att	tat	tgc	tat	cag	gaa	aat	aat	ggg	aag	ccc	atg	gct	961
Phe	Asp	Leu	Ile	Tyr	Cys	Tyr	Gln	Glu	Asn	Asn	Gly	Lys	Pro	Met	Ala	
		305					310					315				
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Leu	Asn	Ala	Gly	Val	Lys	Ala	Cys	Arg	Gly	Asp	Tyr	Ile	Phe	Ile	Val	
	320					325					330					
gac	agt	gat	gat	gca	cta	act	ccc	gat	gcc	ata	aaa	tta	att	aaa	gaa	1057
Asp	Ser	Asp	Asp	Ala	Leu	Thr	Pro	Asp	Ala	Ile	Lys	Leu	Ile	Lys	Glu	
335					340					345				350		
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Ser	Ile	His	Asp	Cys	Leu	Ser	Glu	Lys	Glu	Ser	Phe	Ser	Gly	Val	Gly	
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Phe	Arg	Lys	Ala	Tyr	Ile	Lys	Gly	Gly	Ile	Ile	Gly	Asn	Asp	Leu	Asn	
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Asn	Ser	Ser	Glu	His	Ile	Tyr	Tyr	Leu	Asn	Ala	Thr	Glu	Ile	Ser	Asn	
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 Lys Asn Pro Phe Pro Arg Ile Glu Asp Glu Lys Phe Val Pro Glu Leu
 415 420 425 430

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 Tyr Ile Trp Asn Lys Ile Thr Asp Lys Ala Lys Ile Arg Phe Asn Ile
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agc aaa gtt ata tat ctt tgt gag tat ctt gat gat ggt ctt tct aaa 1393
 Ser Lys Val Ile Tyr Leu Cys Glu Tyr Leu Asp Asp Gly Leu Ser Lys
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 Asn Phe His Asn Gln Leu Lys Lys Tyr Pro Lys Gly Phe Lys Ile Tyr
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tac aaa gat caa aga aaa cga gag aaa act tat ata aaa aaa aca aag 1489
 Tyr Lys Asp Gln Arg Lys Arg Glu Lys Thr Tyr Ile Lys Lys Thr Lys
 480 485 490

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 Met Leu Ile Arg Tyr Leu Gln Cys Cys Tyr Tyr Glu Lys Ile Met
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 Gln Val Cys Leu Leu Ala Asp Lys Leu Ser Leu Ser Gly His His Val
 530 535 540

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 Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn Phe
 575 580 585

aaa cca gac att gta cac agt cat atg ttt cat gca aac att atc act 1824

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Ala	His	Asn	Lys	Asn	Glu	Gly	Gly	Tyr	Phe	Arg	Met	Leu	Thr	Tyr	Arg	
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Leu	Leu	Leu	Ala	Ala	Gly	Arg	Leu	Thr	Leu	Ala	Lys	Asp	Tyr	Pro	Asn	
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Ile	Gly	Asp	Gly	Glu	Leu	Arg	Asp	Glu	Ile	Asn	Met	Leu	Ile	Lys	Lys	
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gct	ccc	tat	ttt	tct	gca	tgt	gat	att	ttt	gtt	ctc	tct	tct	cgt	tgg	2352
Ala	Pro	Tyr	Phe	Ser	Ala	Cys	Asp	Ile	Phe	Val	Leu	Ser	Ser	Arg	Trp	
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Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg Ile
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 Val Val Gly Thr Asp Ser Gly Gly Val Arg Glu Val Ile Gly Asp Asp
 800 805 810
 gat ttt ctt gta ccc ata tct gat tca aca caa ctt gca agc aaa att 2496
 Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys Ile
 815 820 825
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 Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg Asn
 830 835 840 845
 cgt gag cgt att tta aaa aat ttc tca ata gat act att att atg cag 2592
 Arg Glu Arg Ile Leu Lys Asn Phe Ser Ile Asp Thr Ile Ile Met Gln
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 Trp Gln Glu Leu Tyr Gly Thr Ile Ile Cys Ser Lys His Glu Arg
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 Gln Arg Val Thr Leu Asn Glu Ile Ser Ala Leu Tyr Thr Asp Tyr Asp
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gaa tat gat gtc gat tgt cat tgt atc ccc gaa ctt acg aga gaa att 3185
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acc gta aag aat gat ttt aaa gca ttg ttc aag ctt tat aag ttc ata 3233
 Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu Tyr Lys Phe Ile
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 His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser Ser Lys Lys Ser
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 Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys Phe Phe Thr Asp
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aag tta atc gtc ttg aat gta gat gat gaa tat ata gca ata aac aaa 3473
 Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile Ala Ile Asn Lys
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tta aaa ttc aag cgg gat aaa gtt ttt tta att cct aat gga gta gac 3521
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act gat aag ttt tct cct tta gaa aat aaa att tat agt agc acc ttg 3569
 Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr Ser Ser Thr Leu
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 Ile Val Asn Ile Leu Lys Val Asn Asp Leu Phe Ile Leu Pro Ser Leu
 1140 1145 1150

tgg gag ggt atg cca tta gca att tta gaa gca ttg agc tgt gga ctt 3857
 Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu Ser Cys Gly Leu
 1155 1160 1165

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ggc tat aat ggt tgt ttg ttt gaa att aga gat tgt cag tta tta tct 3953
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aaaaagaaca ggtttttcaa agtgaaaata aaattacagt tttttttattg caatgattaa 4162

cgtaacatct gcattacatt caagccgcac aaccccgagg tgaccacccc tgacaggagt 4222

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25

30

Asp Ile Trp Leu Glu Asn Lys Ile Phe Glu Leu Val Lys Tyr Ala Asn

35

40

45

Glu Ile Lys Leu Asn Val Ser Asp Ala Pro Ser Leu Val Tyr Ala Asp

50

55

60

Gly Tyr Ala Tyr Met Asp Gly Glu Gly Thr Ile Asp Phe Ser Gly Ile

65

70

75

80

Ser Asn Asn His Ala Asp Gln Leu Lys Asp Phe Leu Phe Phe Asn Gly

85

90

95

Gly Tyr Gln Gly Cys Ser Ile Met Phe Asn Arg Ala Met Thr Lys Phe

100

105

110

Leu Leu Asn Tyr Arg Gly Phe Val Tyr Leu His Asp Asp Ile Thr Thr

115

120

125

Leu Ala Ala Tyr Ala Leu Gly Lys Val Tyr Phe Leu Pro Lys Tyr Leu

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135

140

Met Leu Tyr Arg Gln His Thr Asn Ala Val Thr Gly Ile Lys Thr Phe

145

150

155

160

Arg Asn Gly Leu Thr Ser Lys Phe Lys Ser Pro Val Asn Tyr Leu Leu

165

170

175

Ser Arg Lys His Tyr Gln Val Lys Lys Ser Phe Phe Glu Cys Asn Ser

180

185

190

Ser Ile Leu Ser Glu Thr Asn Lys Lys Val Phe Leu Asp Phe Ile Ser

195

200

205

Phe Cys Glu Ser Asn Asn Lys Phe Thr Asp Phe Phe Lys Leu Trp Arg
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Ile Ile Ile Asp Asp Gly Ser Ile Asp Ala Thr Ala Val Leu Val Glu
 35 40 45

Asp Phe Arg Lys Lys Cys Asp Phe Asp Leu Ile Tyr Cys Tyr Gln Glu
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Asn Asn Gly Lys Pro Met Ala Leu Asn Ala Gly Val Lys Ala Cys Arg
 65 70 75 80

Gly Asp Tyr Ile Phe Ile Val Asp Ser Asp Asp Ala Leu Thr Pro Asp
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Ala Ile Lys Leu Ile Lys Glu Ser Ile His Asp Cys Leu Ser Glu Lys
 100 105 110

Glu Ser Phe Ser Gly Val Gly Phe Arg Lys Ala Tyr Ile Lys Gly Gly
 115 120 125

Ile Ile Gly Asn Asp Leu Asn Asn Ser Ser Glu His Ile Tyr Tyr Leu
 130 135 140

Asn Ala Thr Glu Ile Ser Asn Leu Ile Asn Gly Asp Val Ala Tyr Cys
 145 150 155 160

Phe Lys Lys Glu Ser Leu Val Lys Asn Pro Phe Pro Arg Ile Glu Asp

165 170 175
 Glu Lys Phe Val Pro Glu Leu Tyr Ile Trp Asn Lys Ile Thr Asp Lys
 180 185 190
 Ala Lys Ile Arg Phe Asn Ile Ser Lys Val Ile Tyr Leu Cys Glu Tyr
 195 200 205
 Leu Asp Asp Gly Leu Ser Lys Asn Phe His Asn Gln Leu Lys Lys Tyr
 210 215 220
 Pro Lys Gly Phe Lys Ile Tyr Tyr Lys Asp Gln Arg Lys Arg Glu Lys
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 Tyr Tyr Glu Lys Ile
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 35 40 45
 Ser Glu Asn Asn Val Asn Val Ile Asn Val Asn Met Ser Lys Asn Ile
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 Ser Gly Val Ile Lys Gly Cys Val Arg Ile Arg Asp Val Ile Ala Asn
 65 70 75 80
 Phe Lys Pro Asp Ile Val His Ser His Met Phe His Ala Asn Ile Ile
 85 90 95
 Thr Arg Leu Ser Val Ile Gly Ile Lys Asn Arg Pro Gly Ile Ile Ser
 100 105 110

Thr Ala His Asn Lys Asn Glu Gly Gly Tyr Phe Arg Met Leu Thr Tyr
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Arg Ile Thr Asp Cys Leu Ser Asp Cys Cys Thr Asn Val Ser Lys Glu
 130 135 140

Ala Val Asp Glu Phe Leu Arg Ile Lys Ala Phe Asn Pro Ala Lys Ala
 145 150 155 160

Ile Thr Met Tyr Asn Gly Ile Asp Thr Asn Lys Phe Lys Phe Asp Leu
 165 170 175

Leu Ala Arg Arg Glu Ile Arg Asp Gly Ile Asn Ile Lys Asn Asp Asp
 180 185 190

Ile Leu Leu Leu Ala Ala Gly Arg Leu Thr Leu Ala Lys Asp Tyr Pro
 195 200 205

Asn Leu Leu Asn Ala Met Thr Leu Leu Pro Glu His Phe Lys Leu Ile
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Ile Ile Gly Asp Gly Glu Leu Arg Asp Glu Ile Asn Met Leu Ile Lys
 225 230 235 240

Lys Leu Gln Leu Ser Asn Arg Val Ser Leu Leu Gly Val Lys Lys Asn
 245 250 255

Ile Ala Pro Tyr Phe Ser Ala Cys Asp Ile Phe Val Leu Ser Ser Arg
 260 265 270

Trp Glu Gly Phe Gly Leu Val Val Ala Glu Ala Met Ser Cys Glu Arg
 275 280 285

Ile Val Val Gly Thr Asp Ser Gly Gly Val Arg Glu Val Ile Gly Asp
 290 295 300

Asp Asp Phe Leu Val Pro Ile Ser Asp Ser Thr Gln Leu Ala Ser Lys
 305 310 315 320

Ile Glu Lys Leu Ser Leu Ser Gln Ile Arg Asp His Ile Gly Phe Arg
 325 330 335

Asn Arg Glu Arg Ile Leu Lys Asn Phe Ser Ile Asp Thr Ile Ile Met
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 35 40 45

Lys Ala Leu Leu Glu Tyr Asp Val Asp Cys His Cys Ile Pro Glu Leu
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Thr Arg Glu Ile Thr Val Lys Asn Asp Phe Lys Ala Leu Phe Lys Leu
 65 70 75 80

Tyr Lys Phe Ile Lys Lys Glu Lys Phe Asp Ile Val His Thr His Ser
 85 90 95

Ser Lys Thr Gly Ile Leu Gly Arg Val Ala Ala Lys Leu Ala Arg Val
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Gly Lys Val Ile His Thr Val His Gly Phe Ser Phe Pro Ala Ala Ser
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Ser Lys Lys Ser Tyr Tyr Leu Tyr Phe Phe Met Glu Trp Ile Ala Lys
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Phe Phe Thr Asp Lys Leu Ile Val Leu Asn Val Asp Asp Glu Tyr Ile
 145 150 155 160

Ala Ile Asn Lys Leu Lys Phe Lys Arg Asp Lys Val Phe Leu Ile Pro
 165 170 175

Asn Gly Val Asp Thr Asp Lys Phe Ser Pro Leu Glu Asn Lys Ile Tyr
 180 185 190

Ser Ser Thr Leu Asn Leu Val Met Val Gly Arg Leu Ser Lys Gln Lys
 195 200 205

Asp Pro Glu Thr Leu Leu Leu Ala Val Glu Lys Leu Leu Asn Glu Asn
 210 215 220

Val Asn Val Lys Leu Thr Leu Val Gly Asp Gly Glu Leu Lys Glu Gln
225 230 235 240

Leu Glu Ser Arg Phe Lys Arg Gln Asp Gly Arg Ile Ile Phe His Gly
245 250 255

Trp Ser Asp Asn Ile Val Asn Ile Leu Lys Val Asn Asp Leu Phe Ile
260 265 270

Leu Pro Ser Leu Trp Glu Gly Met Pro Leu Ala Ile Leu Glu Ala Leu
275 280 285

Ser Cys Gly Leu Pro Cys Ile Val Thr Asn Ile Pro Gly Asn Asn Ser
290 295 300

Leu Ile Glu Asp Gly Tyr Asn Gly Cys Leu Phe Glu Ile Arg Asp Cys
305 310 315 320

Gln Leu Leu Ser Gln Lys Ile Met Ser Tyr Val Gly Lys Pro Glu Leu
325 330 335

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1 5 10 15

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Gln Arg Cys Asp Leu Ile Ala Val Ile Asp Lys Gly Leu Leu Ala Glu
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tac gga acc cac gaa cag ctg tta tct gcg ggc ggc ctc tat acc cgc 143
Tyr Gly Thr His Glu Gln Leu Leu Ser Ala Gly Gly Leu Tyr Thr Arg
      35      40      45

tta tgg cat gac agc gtc agc agt act gct ctc cat cgc cag cac aac 191
Leu Trp His Asp Ser Val Ser Ser Thr Ala Leu His Arg Gln His Asn
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Met Lys Glu Glu Thr Pro Gly
      65      70

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ttaaagagta tga atg ctg aac atg caa caa cat ctc tct gct atc gcc 354
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agc ctg cgc aac caa ctg gca gcg ggc cac att gct aac ctt act gac 402
Ser Leu Arg Asn Gln Leu Ala Ala Gly His Ile Ala Asn Leu Thr Asp
      85      90      95

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Phe Trp Arg Glu Ala Glu Ser Leu Asn Val Pro Leu Val Thr Pro Val
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Glu Gly Ala Glu Asp Glu Arg Glu Val Thr Phe Leu Trp Arg Ala Arg
      120      125      130

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His Pro Leu Gln Gly Val Tyr Leu Arg Leu Asn Arg Val Thr Asp Lys
      135      140      145

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Glu His Val Glu Lys Gly Met Met Ser Ala Leu Pro Glu Thr Asp Ile
      150      155      160

tgg aca ctg aca ctg cgt tta ccc gca agt tac tgc ggc tcc tat tcg 642
Trp Thr Leu Thr Leu Arg Leu Pro Ala Ser Tyr Cys Gly Ser Tyr Ser
      165      170      175

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atg ccg gag atc aac gtt cgg gga aac gca aag gaa tca gtg ctg aca				786
Met Pro Glu Ile Asn Val Arg Gly Asn Ala Lys Glu Ser Val Leu Thr				
215		220	225	
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Leu Asp Lys Ala Pro Ala Leu Ser Glu Trp Asn Gly Gly Phe His Thr				
230		235	240	
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Gly Gln Leu Leu Thr Ser Met Arg Ile Ile Ala Gly Lys Ser Arg Gln				
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Val Arg Leu Tyr Ile Pro Asp Val Asp Ile Ser Gln Pro Leu Gly Leu				
260		265	270	275
gtc gtg ctg ccc gat ggt gaa acc tgg ttt gat cac ctt ggc gta tgc				978
Val Val Leu Pro Asp Gly Glu Thr Trp Phe Asp His Leu Gly Val Cys				
280		285	290	
gcg gca att gac gcc gcc ata aat aat ggg cgc atc gtg ccc gtg gct				1026
Ala Ala Ile Asp Ala Ala Ile Asn Asn Gly Arg Ile Val Pro Val Ala				
295		300	305	
gta ctg ggc att gac aac att aat gaa cat gaa cgc act gag ata ctc				1074
Val Leu Gly Ile Asp Asn Ile Asn Glu His Glu Arg Thr Glu Ile Leu				
310		315	320	
ggc ggg cgc agc aaa ctg ata aag gat atc gcc gga cat ctg ctg ccg				1122
Gly Gly Arg Ser Lys Leu Ile Lys Asp Ile Ala Gly His Leu Leu Pro				
325		330	335	
atg att cgc gct gaa caa ccg cag cgt cag tgg gca gac cgt tcg cgc				1170
Met Ile Arg Ala Glu Gln Pro Gln Arg Gln Trp Ala Asp Arg Ser Arg				
340		345	350	355
aca gtg ctg gcc ggg cag agc ctc ggc ggg atc agt gcg cta atg ggg				1218
Thr Val Leu Ala Gly Gln Ser Leu Gly Gly Ile Ser Ala Leu Met Gly				
360		365	370	
gct cgt tac gca ccg gaa acg ttc ggt ctg gtg ctc agc cac tct cct				1266
Ala Arg Tyr Ala Pr Glu Thr Phe Gly Leu Val Leu Ser His Ser Pro				

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380

385

caa tgc
Gln

1272

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<213> Escherichia coli

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Gly Thr His Glu Gln Leu Leu Ser Ala Gly Gly Leu Tyr Thr Arg Leu
35 40 45

Trp His Asp Ser Val Ser Ser Thr Ala Leu His Arg Gln His Asn Met
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Lys Glu Glu Thr Pro Gly
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<210> 29

<211> 317

<212> PRT

<213> Escherichia coli

<400> 29

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Gln Leu Ala Ala Gly His Ile Ala Asn Leu Thr Asp Phe Trp Arg Glu
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Ala Glu Ser Leu Asn Val Pro Leu Val Thr Pro Val Glu Gly Ala Glu
35 40 45

Asp Glu Arg Glu Val Thr Phe Leu Trp Arg Ala Arg His Pro Leu Gln
50 55 60

Gly Val Tyr Leu Arg Leu Asn Arg Val Thr Asp Lys Glu His Val Glu
65 70 75 80

Lys Gly Met Met Ser Ala Leu Pro Glu Thr Asp Ile Trp Thr Leu Thr
 85 90 95

Leu Arg Leu Pro Ala Ser Tyr Cys Gly Ser Tyr Ser Leu Leu Glu Ile
 100 105 110

Pro Pro Gly Thr Thr Ala Glu Thr Ile Ala Leu Ser Gly Gly Arg Phe
 115 120 125

Ala Thr Leu Ala Gly Lys Ala Asp Pro Leu Asn Lys Met Pro Glu Ile
 130 135 140

Asn Val Arg Gly Asn Ala Lys Glu Ser Val Leu Thr Leu Asp Lys Ala
 145 150 155 160

Pro Ala Leu Ser Glu Trp Asn Gly Gly Phe His Thr Gly Gln Leu Leu
 165 170 175

Thr Ser Met Arg Ile Ile Ala Gly Lys Ser Arg Gln Val Arg Leu Tyr
 180 185 190

Ile Pro Asp Val Asp Ile Ser Gln Pro Leu Gly Leu Val Val Leu Pro
 195 200 205

Asp Gly Glu Thr Trp Phe Asp His Leu Gly Val Cys Ala Ala Ile Asp
 210 215 220

Ala Ala Ile Asn Asn Gly Arg Ile Val Pro Val Ala Val Leu Gly Ile
 225 230 235 240

Asp Asn Ile Asn Glu His Glu Arg Thr Glu Ile Leu Gly Gly Arg Ser
 245 250 255

Lys Leu Ile Lys Asp Ile Ala Gly His Leu Leu Pro Met Ile Arg Ala
 260 265 270

Glu Gln Pro Gln Arg Gln Trp Ala Asp Arg Ser Arg Thr Val Leu Ala
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 Ser Glu Thr Asp Thr Ser Trp Val Ser Glu His Leu Leu Ser Ala Pro
 20 25 30

ccg cag ggc gta cgt atc agc ctg tgc gtg gga tcg ctg gaa ggt tcg 144
 Pro Gln Gly Val Arg Ile Ser Leu Cys Val Gly Ser Leu Glu Gly Ser
 35 40 45

aca gtg cct cac gtt cag cag ctt cac cag cgg ctg att acc gct ggc 192
 Thr Val Pro His Val Gln Gln Leu His Gln Arg Leu Ile Thr Ala Gly
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 Val Glu Ser His Cys Ala Ile Tyr Thr Gly Gly His Asp Tyr Ala Trp
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 Trp Arg Gly Ala Leu Ile Asp Gly Ile Gly Leu Leu Gln Gly
 85 90 95

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ctgcggaaaaa ggaataatca tcag atg tat gcc cgc gag tat cgc tca aca 396
 Met Tyr Ala Arg Glu Tyr Arg Ser Thr
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cgc ccg cat aaa gcg att ttc ttt cat ctt tct tgc ctc acc ctt atc 444
 Arg Pro His Lys Ala Ile Phe Phe His Leu Ser Cys Leu Thr Leu Ile
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 Cys Ser Ala Gln Val Tyr Ala Lys Pro Asp Met Arg Pro Leu Gly Pro
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aat ata gcc gat aaa ggc tcc gtg ttt tac cat ttc agc gtc acc tct 540
 Asn Ile Ala Asp Lys Gly Ser Val Phe Tyr His Phe Ser Val Thr Ser
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 Phe Asp Ser Val Asp Gly Thr Arg His Tyr Arg Val Trp Thr Ala Val
 155 160 165

ccg aat aca acc gca ccg gca tcg ggt tac ccg att tta tat atg ctt 636
 Pro Asn Thr Thr Ala Pro Ala Ser Gly Tyr Pro Ile Leu Tyr Met Leu
 170 175 180

gac ggt aac gca gtt atg gat cgc ctg gat gac gaa ctg ctc aaa caa 684
 Asp Gly Asn Ala Val Met Asp Arg Leu Asp Asp Glu Leu Leu Lys Gln
 185 190 195 200

ttg tca gaa aaa aca ccg cca gtg atc gtg gct gtc ggg tat cag acc 732
 Leu Ser Glu Lys Thr Pro Pro Val Ile Val Ala Val Gly Tyr Gln Thr
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 Asn Leu Pro Phe Asp Leu Asn Ser Arg Ala Tyr Asp Tyr Thr Pro Ala
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gca gaa agc aga aaa aca gat ctc cac tca ggg cgt ttt agc cgt aag 828
 Ala Glu Ser Arg Lys Thr Asp Leu His Ser Gly Arg Phe Ser Arg Lys
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 Ser Ser Tyr Phe Arg Ser Tyr Tyr Ser Ala Ser Pro Ser Leu Gly Arg
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ggt tat gat gct ttg cta agc cgc gtt acg gcg gtt gag cct ctg caa 1068
 Gly Tyr Asp Ala Leu Leu Ser Arg Val Thr Ala Val Glu Pro Leu Gln
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 Phe Cys Ala Lys His Leu Ala Ile Met Glu Gly Ser Ala Thr Gln Gly
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gat aac cgg gaa acg cat gct gtc ggg gtg ctg tcg aaa att cat acc 1164
 Asp Asn Arg Glu Thr His Ala Val Gly Val Leu Ser Lys Ile His Thr
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acc ctc act ata ctg aaa gat aaa ggc gtc aat gcc gta ttt tgg gat 1212
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gca ctg tta gat atc agt ggt gaa aac gca aat tac aca gca ggt tgt 1308
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<211> 94

<212> PRT

<213> Escherichia coli

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Pro Gln Gly Val Arg Ile Ser Leu Cys Val Gly Ser Leu Glu Gly Ser
 35 40 45

Thr Val Pro His Val Gln Gln Leu His Gln Arg Leu Ile Thr Ala Gly
 50 55 60

Val Glu Ser His Cys Ala Ile Tyr Thr Gly Gly His Asp Tyr Ala Trp
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<400> 32

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 35 40 45

Val Phe Tyr His Phe Ser Val Thr Ser Phe Asp Ser Val Asp Gly Thr
 50 55 60

Arg His Tyr Arg Val Trp Thr Ala Val Pro Asn Thr Thr Ala Pro Ala
 65 70 75 80

Ser Gly Tyr Pro Ile Leu Tyr Met Leu Asp Gly Asn Ala Val Met Asp
 85 90 95

Arg Leu Asp Asp Glu Leu Leu Lys Gln Leu Ser Glu Lys Thr Pro Pro
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Val Ile Val Ala Val Gly Tyr Gln Thr Asn Leu Pro Phe Asp Leu Asn
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Ser Arg Ala Tyr Asp Tyr Thr Pro Ala Ala Glu Ser Arg Lys Thr Asp
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Leu His Ser Gly Arg Phe Ser Arg Lys Ser Gly Gly Ser Asn Asn Phe
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Arg Gln Leu Leu Glu Thr Arg Ile Ala Pro Lys Val Glu Gln Gly Leu
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Asn Ile Asp Arg Gln Arg Arg Gly Leu Trp Gly His Ser Tyr Gly Gly
 180 185 190

Leu Phe Val Leu Asp Ser Trp Leu Ser Ser Ser Tyr Phe Arg Ser Tyr
 195 200 205

Tyr Ser Ala Ser Pro Ser Leu Gly Arg Gly Tyr Asp Ala Leu Leu Ser
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Arg Val Thr Ala Val Glu Pro Leu Gln Phe Cys Ala Lys His Leu Ala
225 230 235 240

Ile Met Glu Gly Ser Ala Thr Gln Gly Asp Asn Arg Glu Thr His Ala
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Val Gly Val Leu Ser Lys Ile His Thr Thr Leu Thr Ile Leu Lys Asp
260 265 270

Lys Gly Val Asn Ala Val Phe Trp Asp Phe Pro Asn Leu Gly His Gly
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<211> 3292

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15

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25

30

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50

55

60

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65

70

75

80

gaa gtg atc gcg tca gcc att gcg aaa agc ctc tac ccg ggc gta gat 289
 Glu Val Ile Ala Ser Ala Ile Ala Lys Ser Leu Tyr Pro Gly Val Asp

85

90

95

ccg tcg aaa ctg aca gaa gat cag aag caa act gta agc acg ctg gca 337
 Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala

100

105

110

acg ctg tca gcg ggt atg gcc ggc ggc att gcc agt ggc gat gtg gct 385
 Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala

115

120

125

ggc gcg gct gct gga gct ggt gcc ggc aag aac gtt gtt gag aat aat 433
 Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn

130

135

140

gcg ctg agt ctg gtt gcc aga ggc tgt gcg gtc gca gca cct tgc agg 481
 Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg

145

150

155

160

act aaa gtt gca gag cag ttg cta gaa atc ggg gcg aaa gcg ggc atg 529
 Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met

165

170

175

gcc ggc ctt gcc ggc gcg gca gtc aag gat atg gcc gac agg atg acc 577
 Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr

180

185

190

tcc gat gaa ctg gag cat ctg att acc ctg caa atg atg ggt aat gat 625
 Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp
 195 200 205

gag atc act act aag tat ctc agt tcg ttg cat gat aag tac ggt tcc 673
 Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser
 210 215 220

ggg gct gcc tcg aat ccg aat atc ggt aaa gat ctg acc gat gcg gaa 721
 Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu
 225 230 235 240

aaa gta gaa ctg ggc ggt tcc ggc tca gga acc ggt aca cca cca cca 769
 Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro
 245 250 255

tcg gaa aat gat cct aag cag caa aat gaa aaa act gta gat aag ctt 817
 Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu
 260 265 270

aat cag aag caa gaa agt gcg att aag aag atc gat aac act ata aaa 865
 Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys
 275 280 285

aat gct ctg aaa gat cat gat att att gga act ctc aag gat atg gat 913
 Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp
 290 295 300

ggt aag cca gtt cct aaa gag aat gga gga tat tgg gat cat atg cag 961
 Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln
 305 310 315 320

gaa atg caa aat acg ctc aga gga tta aga aat cat gcg gat acg ttg 1009
 Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu
 325 330 335

aaa aac gtc aac aat cct gaa gct cag gct gcg tat ggc aga gca aca 1057
 Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr
 340 345 350

gat gct att aat aaa ata gaa tca gcc ttg aaa gga tat gga at atg 1104
 Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly Met
 355 360 365

att acc tta cgt aaa ttg att gga aac atc aat atg aca aaa gag cct 1152
 Ile Thr Leu Arg Lys Leu Ile Gly Asn Ile Asn Met Thr Lys Glu Pro
 370 375 380

gag caa caa tca ccg ctt gaa ctc tgg ttc gaa cgt atc ata gat gtg 1200
 Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp Val
 385 390 395

cct ctt gaa aag tta aca gtg gaa gat ctt tgc cgc gct atc cga caa 1248
 Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg Gln
 400 405 410 415

aat tta tgt att gat cag ttg atg cca aga gtg ttg gaa gtt cta act 1296
 Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu Thr
 420 425 430

aaa gag ccg tta gcg ggt gaa tat tac gat ggt gaa cta att gca gct 1344
 Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala Ala
 435 440 445

tta tca acg ata aaa gga gaa gat cta aaa gat cag aaa agt acc ttt 1392
 Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr Phe
 450 455 460

acc caa ata agg caa ctt ata aac cag cta gaa ccg tca gat att aac 1440
 Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile Asn
 465 470 475

gat gat tta aga aaa gat ata tta aaa atc aat cag ata att gta 1485
 Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val
 480 485 490

taactaatcc cggccactga gccgagatct tctttgtgtg ccgggcatgt tcagcagctt 1545

gggggtgaaa gtccctgtc cagcctg atg gtg gcg aag gcg ttc gcg tac gca 1599
 Met Val Ala Lys Ala Phe Ala Tyr Ala
 495 500

ctt aac cag tgg ccg gca ctg acg tac tat gcg aac gat ggc tgg gtg 1647
 Leu Asn Gln Trp Pro Ala Leu Thr Tyr Tyr Ala Asn Asp Gly Trp Val
 505 510 515

gaa atc gac aac aac atc gct gaa aat gcc ctg cgg gcg gtc agt ctg 1695
 Glu Ile Asp Asn Asn Ile Ala Glu Asn Ala Leu Arg Ala Val Ser Leu
 520 525 530 535

ggt cgt aaa aac ttc ctg ttc ttc ggc tct gac cat ggt ggt gag cgg 1743
 Gly Arg Lys Asn Phe Leu Phe Phe Gly Ser Asp His Gly Gly Glu Arg
 540 545 550

gga gcg cta ctg tac agc ctg atc ggg acg tgc aaa ctg aat gac gtg 1791

Gly Ala Leu Leu Tyr Ser Leu Ile Gly Thr Cys Lys Leu Asn Asp Val
 555 560 565

gat cca gaa agc tac ctt cgc cat gtg ctt gcc gtc ata gca gac tgg 1839
 Asp Pro Glu Ser Tyr Leu Arg His Val Leu Ala Val Ile Ala Asp Trp
 570 575 580

ccg gtc aac cgg gtc agc gaa ctg ctt ccg tgg cgc ata gca ctg cca 1887
 Pro Val Asn Arg Val Ser Glu Leu Leu Pro Trp Arg Ile Ala Leu Pro
 585 590 595

gct gaa taacacatcc ccgtcaatac ggccctcgct gtacgcttac agaaa atg ctg 1944
 Ala Glu Met Leu
 600

atg tct gta cag aaa gaa aag aac gtc gca gag agt gtg gta tct gaa 1992
 Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val Ser Glu
 605 610 615

acg cat acc ggc gac agc gta tat gct tcc ctg ttt gaa aaa att aac 2040
 Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys Ile Asn
 620 625 630 635

ctg aat ccg gta tct gcc ctg agt gca ctg gat aac cct ttc cgg tca 2088
 Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe Arg Ser
 640 645 650

gca gat aac gcg act ggc aga att acc tcc agc ata caa cct gcg gtg 2136
 Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro Ala Val
 655 660 665

cag tgc gca gct gct gca gca act gag ggt tct tgt ccc cgg caa tcc 2184
 Gln Cys Ala Ala Ala Ala Ala Thr Glu Gly Ser Cys Pro Arg Gln Ser
 670 675 680

ccg tgt tca gga a atg gtg gat aac tgg cag aag agt gta agg agt cgt 2233
 Pro Cys Ser Gly Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg
 685 690 695

gcg ctc ccg gaa gag gcg atg acg ggc tgg aac gaa ggc atg atc cgc 2281
 Ala Leu Pro Glu Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg
 700 705 710 715

tta cag cag ttg gct gag cgc ctg aac cgt cag gat gaa cag cgg gga 2329
 Leu Gln Gln Leu Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly
 720 725 730

aaa tac atg acg gtc agt gaa ctg aaa acg gag gtg ttt ggc atc atg 2377

Lys Tyr Met Thr Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met
 735 740 745
 cag gct ttt aac cgg cat atc ccg gcg gaa gag cag tta cgt cgc tac 2425
 Gln Ala Phe Asn Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr
 750 755 760
 ggt gaa gtc cgt aac cag aat ggc agt gaa cag cag caa aaa cag gct 2473
 Gly Glu Val Arg Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala
 765 770 775
 gaa atg gcg cta aat cag tta att aac cgt tat cag atg ata cgt gca 2521
 Glu Met Ala Leu Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala
 780 785 790 795
 ggc aaa caa tagtggtagc cataatgcag gagcaaagcc tgaatcagga 2570
 Gly Lys Gln
 agagttattc tgactgagtt tggttttctg gcgattcttg tg atg gtg gga tgt 2624
 Met Val Gly Cys
 800
 gct tgg tta gct gaa cag gcc ttt tcc gac cat gcg ctt tca cca cac 2672
 Ala Trp Leu Ala Glu Gln Ala Phe Ser Asp His Ala Leu Ser Pro His
 805 810 815
 agt gct tgg ccg tac agt gca tcg cgc gat gcc ggg ctg gcc gat acg 2720
 Ser Ala Trp Pro Tyr Ser Ala Ser Arg Asp Ala Gly Leu Ala Asp Thr
 820 825 830
 ggc gcg ggc ggc tat ccc act tgt aaa cag cgg tgg gcc gac gac acc 2768
 Gly Ala Gly Gly Tyr Pro Thr Cys Lys Gln Arg Trp Ala Asp Asp Thr
 835 840 845 850
 gtt ggg ctg aaa gcc cgt cta ctg caa ctt cct gcc cta gat atc tgg 2816
 Val Gly Leu Lys Ala Arg Leu Leu Gln Leu Pro Ala Leu Asp Ile Trp
 855 860 865
 acg gcg ttt aaa aaa atc gac cag tcg cag gta gtg tat gaa gag gcc 2864
 Thr Ala Phe Lys Lys Ile Asp Gln Ser Gln Val Val Tyr Glu Glu Ala
 870 875 880
 gtg ctg cgc tcg cgg gtc agt gaa cga aat atg cag gta tcg cag aat 2912
 Val Leu Arg Ser Arg Val Ser Glu Arg Asn Met Gln Val Ser Gln Asn
 885 890 895
 ggg cgc gtt tat cca agc tat ggc ggt aac gtt gat ggc acc gtc gcc 2960
 Gly Arg Val Tyr Pro Ser Tyr Gly Gly Asn Val Asp Gly Thr Val Ala

900	905	910	
aat gcc gcc acc cgg ttg gca tcc ggc gct aga aat atc ctc ggc agc			3008
Asn Ala Ala Thr Arg Leu Ala Ser Gly Ala Arg Asn Ile Leu Gly Ser			
915	920	925	930
ata gcg gca tgt acg gca ttc gac agc gtg cgt taggcactac cg atg gta			3059
Ile Ala Ala Cys Thr Ala Phe Asp Ser Val Arg			Met Val
935	940		
cag gcg cag ctg caa ata gcg ctg gtg atc tgt att ccg ctg ata acg			3107
Gln Ala Gln Leu Gln Ile Ala Leu Val Ile Cys Ile Pro Leu Ile Thr			
945	950	955	
ctc tgt tcg gcg tgg gat gtg aaa gta gtg atg acg ctg acg ttt gtg			3155
Leu Cys Ser Ala Trp Asp Val Lys Val Val Met Thr Leu Thr Phe Val			
960	965	970	975
cag ttt gca cta ttt ttc ctc acc ttt tgg tgg gaa ctg gca cgg tgg			3203
Gln Phe Ala Leu Phe Phe Leu Thr Phe Trp Trp Glu Leu Ala Arg Trp			
980	985	990	
ctt gat agc tgg ctg ctg gat gtg ctc tac aac agc gat acc cac agt			3251
Leu Asp Ser Trp Leu Leu Asp Val Leu Tyr Asn Ser Asp Thr His Ser			
995	1000	1005	
agc tgg aat tta gcc ggg atc cag aat acg cag gat gac gtg att atc			3299
Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val Ile Ile			
1010	1015	1020	
aat ctg gtg atg agg ttg atg ttt ctg gtg ttg ccg aca ttc tgg ctg			3347
Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe Trp Leu			
1025	1030	1035	
ggg gcg atg acg tgg gct gga gtg agg gtt ggc gtg gcg ctg aat gga			3395
Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu Asn Gly			
1040	1045	1050	1055
gcg ctg gcg gga tgattgggag gtgattcgcc aatctcactt tcctatacac			3447
Ala Leu Ala Gly			
atataaaatg ta atg aaa tat ctc ttt ttt gag aat ata cat tct ata ttt			3498
Met Lys Tyr Leu Phe Phe Glu Asn Ile His Ser Ile Phe			
1060	1065	1070	
tta aca ttc agt ctc ttc cga aca tct gtg tcg cct gat ttc cca atg			3546
Leu Thr Phe Ser Leu Phe Arg Thr Ser Val Ser Pro Asp Phe Pro Met			
1075	1080	1085	

att ttt gca ttg ccc tca atc att tta ggt caa ttt acg acc aac caa 3594
 Ile Phe Ala Leu Pro Ser Ile Ile Leu Gly Gln Phe Thr Thr Asn Gln
 1090 1095 1100

tta act aac ttt gtg ata tgt atg ggt aac acc gtt gaa cgt cgg ctg 3642
 Leu Thr Asn Phe Val Ile Cys Met Gly Asn Thr Val Glu Arg Arg Leu
 1105 1110 1115 1120

ggg gtt gtt cat aat ccc ttt aaa agg tct ggg gat ggc cat gac ctc 3690
 Gly Val Val His Asn Pro Phe Lys Arg Ser Gly Asp Gly His Asp Leu
 1125 1130 1135

agg gcg gta gcg tgaccaaagt tcatatccat accaattatt tttatttaaa 3742
 Arg Ala Val Ala
 1140

atatcaactt attcgagttg ttttatttag ttcaaagaag gtatcaaa ttg ata gtt 3799
 Leu Ile Val

ata gat ttt ttt tgt ggc tgt ggt gga gcc agt gaa ggg cta cgt cag 3847
 Ile Asp Phe Phe Cys Gly Cys Gly Gly Ala Ser Glu Gly Leu Arg Gln
 1145 1150 1155

gct ggc ttt gat atc gag ctt gga tta gat att gac caa caa gca tca 3895
 Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln Gln Ala Ser
 1160 1165 1170 1175

gaa aca ttt aaa gct aat ttc cct gat gca aaa ttc atc caa gat gat 3943
 Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile Gln Asp Asp
 1180 1185 1190

att agg aaa atc gaa cct caa gat atc tcc gac atc att gat att aaa 3991
 Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile Asp Ile Lys
 1195 1200 1205

gct aaa cgg cct ttg tta ctg agt gca tgt gca cca tgt caa cca ttt 4039
 Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys Gln Pro Phe
 1210 1215 1220

tcg caa cag aat aaa aat aaa act agt gac gac tca agg aga aat cta 4087
 Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg Arg Asn Leu
 1225 1230 1235

cta aat gaa act cat cgt ttt att aga gaa ctt ctt cct gaa tat att 4135
 Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro Glu Tyr Ile
 1240 1245 1250 1255

atg ctt gaa aat gtt cct gga atg caa aaa att gat gaa gaa aaa gaa 4183
 Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu Glu Lys Glu
 1260 1265 1270

ggc cca ttt cag gag ttt att aag cta ctt aaa gag tta gag tat aac 4231
 Gly Pro Phe Gln Glu Phe Ile Lys Leu Leu Lys Glu Leu Glu Tyr Asn
 1275 1280 1285

tat ata tct ttt ata gcc aat gct gag aac tat ggg att ccc caa aga 4279
 Tyr Ile Ser Phe Ile Ala Asn Ala Glu Asn Tyr Gly Ile Pro Gln Arg
 1290 1295 1300

aga aaa aga ctc gtg ctc tta gct agt cga gta ggt aaa gtt acc cta 4327
 Arg Lys Arg Leu Val Leu Leu Ala Ser Arg Val Gly Lys Val Thr Leu
 1305 1310 1315

cca gag ata acc cat ggt aaa aat aaa atc cca ttc aaa act gta cga 4375
 Pro Glu Ile Thr His Gly Lys Asn Lys Ile Pro Phe Lys Thr Val Arg
 1320 1325 1330 1335

gat tat atc cag gac ttc aca aag tta tgt tca gga gaa acc gac ccc 4423
 Asp Tyr Ile Gln Asp Phe Thr Lys Leu Cys Ser Gly Glu Thr Asp Pro
 1340 1345 1350

aaa gat cct tta cat agg gct gga aca ctg agc cct ctt aac cta aaa 4471
 Lys Asp Pro Leu His Arg Ala Gly Thr Leu Ser Pro Leu Asn Leu Lys
 1355 1360 1365

aga att atg cac act cca gaa gga ggg gat aga aga aat tgg cca gaa 4519
 Arg Ile Met His Thr Pro Glu Gly Gly Asp Arg Arg Asn Trp Pro Glu
 1370 1375 1380

gag tta gtt aat aaa tgc cat aaa aat tat gat ggc cac aca gat act 4567
 Glu Leu Val Asn Lys Cys His Lys Asn Tyr Asp Gly His Thr Asp Thr
 1385 1390 1395

tat gga aga atg agt tgg gat aag cct gcg cct aca ctt acg acg aaa 4615
 Tyr Gly Arg Met Ser Trp Asp Lys Pro Ala Pro Thr Leu Thr Thr Lys
 1400 1405 1410 1415

tgt aat agt tac tcc aat ggt cgt ttt ggg cat cct gac ccc act caa 4663
 Cys Asn Ser Tyr Ser Asn Gly Arg Phe Gly His Pro Asp Pro Thr Gln
 1420 1425 1430

cat aga gca att agc ata aga gaa gca tca aga tta caa aca ttt cct 4711
 His Arg Ala Ile Ser Ile Arg Glu Ala Ser Arg Leu Gln Thr Phe Pro
 1435 1440 1445

tta agc tat gtt ttt aaa ggt tgc ctg aat tca atg gca aag caa atc 4759
 Leu Ser Tyr Val Phe Lys Gly Ser Leu Asn Ser Met Ala Lys Gln Ile
 1450 1455 1460

ggc aat gct gta cct tgc gaa ctc gct aga cta ttt ggg cta cat ctc 4807
 Gly Asn Ala Val Pro Cys Glu Leu Ala Arg Leu Phe Gly Leu His Leu
 1465 1470 1475

ata gaa aat tgt act aat aag gat tca tagatatatg gctaaaataa 4854
 Ile Glu Asn Cys Thr Asn Lys Asp Ser
 1480 1485

gaacaaaggc tcgagctttg gac atg ctt ggc aga caa caa att gca ggt ata 4907
 Met Leu Gly Arg Gln Gln Ile Ala Gly Ile
 1490 1495

cct act gcc ttg agt gag tta ttt aaa aat gct cat gat gcc tat gct 4955
 Pro Thr Ala Leu Ser Glu Leu Phe Lys Asn Ala His Asp Ala Tyr Ala
 1500 1505 1510

gat aat gtc gaa gtt gat ttt ttt agg aaa gaa aat ctt ctt atc ttg 5003
 Asp Asn Val Glu Val Asp Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu
 1515 1520 1525 1530

aga gat gat gga tta ggt atg aca acc gat gaa ttt gaa gag agg tgg 5051
 Arg Asp Asp Gly Leu Gly Met Thr Thr Asp Glu Phe Glu Glu Arg Trp
 1535 1540 1545

ttg act att gga acc tcc agc aaa tta atc gac gat gat gca att aat 5099
 Leu Thr Ile Gly Thr Ser Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn
 1550 1555 1560

aaa cca gca gtg gat agt aat aaa gcc ttt cgc cct atc atg gga gag 5147
 Lys Pro Ala Val Asp Ser Asn Lys Ala Phe Arg Pro Ile Met Gly Glu
 1565 1570 1575

aaa gga ata ggc cgt tta tct atc gca gca att gga cca cag gtg ctg 5195
 Lys Gly Ile Gly Arg Leu Ser Ile Ala Ala Ile Gly Pro Gln Val Leu
 1580 1585 1590

gtt ctt act agg gcc aaa aga gac aat gag ctt aag cca tta gtt gct 5243
 Val Leu Thr Arg Ala Lys Arg Asp Asn Glu Leu Lys Pro Leu Val Ala
 1595 1600 1605 1610

gca ttt gtt aat tgg agt tta ttt gct ata cca tca ctt gat ctt gat 5291
 Ala Phe Val Asn Trp Ser Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp
 1615 1620 1625

gat ata gaa ata cca att aga act att atc aac gac gaa tgc ttc act 5339
Asp Ile Glu Ile Pro Ile Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr
1630 1635 1640

aaa aaa act ctt gat gag atg att gag caa gca aga aat aat tta gac 5387
Lys Lys Thr Leu Asp Glu Met Ile Glu Gln Ala Arg Asn Asn Leu Asp
1645 1650 1655

tct tta tca cac aaa ata tca aaa tca aaa gta tca caa ata aat aca 5435
Ser Leu Ser His Lys Ile Ser Lys Ser Lys Val Ser Gln Ile Asn Thr
1660 1665 1670

caa tta tca tct ttt gaa ttt gat cct att cta tgg gaa aaa aaa tta 5483
Gln Leu Ser Ser Phe Glu Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu
1675 1680 1685 1690

ggg ggg cta aga cta tct gga gat ggg cat gga act cac ttc ata ata 5531
Gly Gly Leu Arg Leu Ser Gly Asp Gly His Gly Thr His Phe Ile Ile
1695 1700 1705

atg cct acc gaa gaa ata tta ata gat gac att tcc acg agc gat agc 5579
Met Pro Thr Glu Glu Ile Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser
1710 1715 1720

aat aaa aca tca gag cag tct tct cgc tta gaa aaa gct tta tta ggt 5627
Asn Lys Thr Ser Glu Gln Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly
1725 1730 1735

ttt aca aac aca atg tac agt gat tca aac cct cct att ata gct cgt 5675
Phe Thr Asn Thr Met Tyr Ser Asp Ser Asn Pro Pro Ile Ile Ala Arg
1740 1745 1750

ttt aga gac tat ctg gaa gat ggt gag tgc att gac aga att agc gaa 5723
Phe Arg Asp Tyr Leu Glu Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu
1755 1760 1765 1770

tca att ttt ttt aca ccg caa gaa ttc aat ctt gca gat cac cac att 5771
Ser Ile Phe Phe Thr Pro Gln Glu Phe Asn Leu Ala Asp His His Ile
1775 1780 1785

gaa gga tgg ttc aat gaa ttt ggt caa ttc agt gga act gtt tct gtt 5819
Glu Gly Trp Phe Asn Glu Phe Gly Gln Phe Ser Gly Thr Val Ser Val
1790 1795 1800

tat ggt gaa gag cca att cat cat gtc gtg act tgg aaa aat aat aat 5867
Tyr Gly Glu Glu Pro Ile His His Val Val Thr Trp Lys Asn Asn Asn
1805 1810 1815

caa tta acc caa tgc ggt cca ttt aaa ata aaa tta gcg tat att cat 5915
 Gln Leu Thr Gln Cys Gly Pro Phe Lys Ile Lys Leu Ala Tyr Ile His
 1820 1825 1830

ggt cgg ctt cgt gat tca cgc tta ccc atg gag ttg tgg gcc cct ctg 5963
 Gly Arg Leu Arg Asp Ser Arg Leu Pro Met Glu Leu Trp Ala Pro Leu
 1835 1840 1845 1850

aag gag aaa aca gat aga tat ggt ggt tta tat atc tat cga gat gga 6011
 Lys Glu Lys Thr Asp Arg Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly
 1855 1860 1865

tta aga att ttg ccc tat gga gat tca gat acg gat ttt cta aaa ata 6059
 Leu Arg Ile Leu Pro Tyr Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile
 1870 1875 1880

gaa aag aga aga acg tta tcc gct tct gaa tat ttt ttc tca tat cga 6107
 Glu Lys Arg Arg Thr Leu Ser Ala Ser Glu Tyr Phe Phe Ser Tyr Arg
 1885 1890 1895

cgt ttg ttt gga gca ata gaa tta aca aaa gaa aac aat gct tca tta 6155
 Arg Leu Phe Gly Ala Ile Glu Leu Thr Lys Glu Asn Asn Ala Ser Leu
 1900 1905 1910

gtt gaa aaa gct ggg cga gaa gga ttc att gaa aat aag cca tat aaa 6203
 Val Glu Lys Ala Gly Arg Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys
 1915 1920 1925 1930

cag ttt aaa gaa atg ctt gaa aat ttc ttc atc gaa atc gca aga gat 6251
 Gln Phe Lys Glu Met Leu Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp
 1935 1940 1945

ttc ttt aag gac gat ggc gat atg tct gaa tta ttt gtt gag aca aag 6299
 Phe Phe Lys Asp Asp Gly Asp Met Ser Glu Leu Phe Val Glu Thr Lys
 1950 1955 1960

caa cgt aga aat gaa gaa cat gat ttg tta tct aaa aga tct aaa caa 6347
 Gln Arg Arg Asn Glu Glu His Asp Leu Leu Ser Lys Arg Ser Lys Gln
 1965 1970 1975

act aaa gct aaa aaa gat aga tta aag aaa gat ctg tat gat ttt ttt 6395
 Thr Lys Ala Lys Lys Asp Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe
 1980 1985 1990

gat aag tta gat aat gat tac tgg aat att gaa ata aat aag cta atc 6443
 Asp Lys Leu Asp Asn Asp Tyr Trp Asn Ile Glu Ile Asn Lys Leu Ile
 1995 2000 2005 2010

aat aaa aac gag gaa tat ttc tcc agt aca gaa ata aca gac acc aat 6491
Asn Lys Asn Glu Glu Tyr Phe Ser Ser Thr Glu Ile Thr Asp Thr Asn
2015 2020 2025

ata gat tat gta tac aat aaa att aaa gaa caa aat gat gct atc att 6539
Ile Asp Tyr Val Tyr Asn Lys Ile Lys Glu Gln Asn Asp Ala Ile Ile
2030 2035 2040

aaa aat cta cgt aat tct gtg gat ata aag aaa ccc tct gga gtt gga 6587
Lys Asn Leu Arg Asn Ser Val Asp Ile Lys Lys Pro Ser Gly Val Gly
2045 2050 2055

tta aca aaa gag tta tct aat tta tgg gat aga tat caa ata gaa aga 6635
Leu Thr Lys Glu Leu Ser Asn Leu Trp Asp Arg Tyr Gln Ile Glu Arg
2060 2065 2070

caa aaa ata ctg tta tca cta aat gag cta aaa gat aac gtt gat aga 6683
Gln Lys Ile Leu Leu Ser Leu Asn Glu Leu Lys Asp Asn Val Asp Arg
2075 2080 2085 2090

aag ctt ata gaa ctg gat aat aaa aat aat gat ttt ctc aac tta cgg 6731
Lys Leu Ile Glu Leu Asp Asn Lys Asn Asn Asp Phe Leu Asn Leu Arg
2095 2100 2105

aag aga ctt gaa gat tct ttg aat cta caa caa agt tac tat gaa aaa 6779
Lys Arg Leu Glu Asp Ser Leu Asn Leu Gln Gln Ser Tyr Tyr Glu Lys
2110 2115 2120

gaa cta aca aag tta tat aat gac gct aaa aat gct ttg aaa gat gtg 6827
Glu Leu Thr Lys Leu Tyr Asn Asp Ala Lys Asn Ala Leu Lys Asp Val
2125 2130 2135

caa tct aaa gca aat agg tta att tct gat aat aag aaa aaa cat aag 6875
Gln Ser Lys Ala Asn Arg Leu Ile Ser Asp Asn Lys Lys Lys His Lys
2140 2145 2150

agt gaa cta aaa aac att tct tat gaa ttc caa tca act aat ctc aat 6923
Ser Glu Leu Lys Asn Ile Ser Tyr Glu Phe Gln Ser Thr Asn Leu Asn
2155 2160 2165 2170

ggc aaa gat act gcg tat ata ttg gat gta aaa aga aat cta gaa agt 6971
Gly Lys Asp Thr Ala Tyr Ile Leu Asp Val Lys Arg Asn Leu Glu Ser
2175 2180 2185

aaa att gag aat act tca aac gaa gtg att aat gaa ata aga aaa cta 7019
Lys Ile Glu Asn Thr Ser Asn Glu Val Ile Asn Glu Ile Arg Lys Leu
2190 2195 2200

acc gac cag att gca ata att agt gat agt acc act tct gaa aat tta 7067
 Thr Asp Gln Ile Ala Ile Ile Ser Asp Ser Thr Thr Ser Glu Asn Leu
 2205 2210 2215

tca tcg gct caa gta act gaa gca atc gaa act gaa ctt gaa cat tta 7115
 Ser Ser Ala Gln Val Thr Glu Ala Ile Glu Thr Glu Leu Glu His Leu
 2220 2225 2230

cga gac caa caa gca aat aac gca gag tta ata cta ctt ggc atg gct 7163
 Arg Asp Gln Gln Ala Asn Asn Ala Glu Leu Ile Leu Leu Gly Met Ala
 2235 2240 2245 2250

ctt tct gta gta cat cat gaa ttt aat ggt aat att agg gca att aga 7211
 Leu Ser Val Val His His Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg
 2255 2260 2265

agt gcg cta agg gaa tta aaa gca tgg gct gac aga aat cct aag ctt 7259
 Ser Ala Leu Arg Glu Leu Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu
 2270 2275 2280

gat att ata tac caa aaa atc aga act agt ttt gat cac tta gat ggt 7307
 Asp Ile Ile Tyr Gln Lys Ile Arg Thr Ser Phe Asp His Leu Asp Gly
 2285 2290 2295

tat tta aaa acc ttt aca cca ttg aca aga cgt tta agt cgc tct aaa 7355
 Tyr Leu Lys Thr Phe Thr Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys
 2300 2305 2310

acc aat ata act gga act gcc att tta gaa ttt atc aga gat gta ttc 7403
 Thr Asn Ile Thr Gly Thr Ala Ile Leu Glu Phe Ile Arg Asp Val Phe
 2315 2320 2325 2330

gat gat cgt ctt gag aaa gaa gga att gaa tta ttc act acc tca aag 7451
 Asp Asp Arg Leu Glu Lys Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys
 2335 2340 2345

ttt gtt aat caa gaa att gta act tac aca tca acc att tac cct gtc 7499
 Phe Val Asn Gln Glu Ile Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val
 2350 2355 2360

ttt ata aat cta att gat aac gca ata tac tgg ctt ggg aaa aca act 7547
 Phe Ile Asn Leu Ile Asp Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr
 2365 2370 2375

gga gaa aaa aga ctt ata ctt gat gct act gaa aca gga ttt gtt att 7595
 Gly Glu Lys Arg Leu Ile Leu Asp Ala Thr Glu Thr Gly Phe Val Ile
 2380 2385 2390

ggt gat act ggt ccc ggt gtt tca act aga gat cga gat ata ata ttt 7643
 Gly Asp Thr Gly Pro Gly Val Ser Thr Arg Asp Arg Asp Ile Ile Phe
 2395 2400 2405 2410

gat atg gga ttt aca cga aaa aca gga ggg cgt gga atg gga tta ttc 7691
 Asp Met Gly Phe Thr Arg Lys Thr Gly Gly Arg Gly Met Gly Leu Phe
 2415 2420 2425

att tcc aaa gag tgt tta tct cga gat gga ttt act ata aga ttg gat 7739
 Ile Ser Lys Glu Cys Leu Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp
 2430 2435 2440

gat tac act cct gaa cag ggt gct ttc ttt att att gag cca tca gaa 7787
 Asp Tyr Thr Pro Glu Gln Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu
 2445 2450 2455

gaa aca agt gaa tag cggatataaaa taa atg aca agc tct act gat ttt 7836
 Glu Thr Ser Glu Met Thr Ser Ser Thr Asp Phe
 2460 2465 2470

cat aaa ctt tct gaa gac tgc gtt cgc cgt ttt tta cat tct gta gtt 7884
 His Lys Leu Ser Glu Asp Cys Val Arg Arg Phe Leu His Ser Val Val
 2475 2480 2485

gct gta gat gac aat atg tct ttt gga gct ggt agt gat act ttc cct 7932
 Ala Val Asp Asp Asn Met Ser Phe Gly Ala Gly Ser Asp Thr Phe Pro
 2490 2495 2500

aca gac gaa gat att aat gct tta gtt gat ccc gac gat gat cct aca 7980
 Thr Asp Glu Asp Ile Asn Ala Leu Val Asp Pro Asp Asp Asp Pro Thr
 2505 2510 2515

cca ata ata aca gca tca gca tcc cca agg ata gaa tca act aaa tca 8028
 Pro Ile Ile Thr Ala Ser Ala Ser Pro Arg Ile Glu Ser Thr Lys Ser
 2520 2525 2530

aaa gca aag gta aaa aac cat cct ttt gat tac caa gct cta gca gaa 8076
 Lys Ala Lys Val Lys Asn His Pro Phe Asp Tyr Gln Ala Leu Ala Glu
 2535 2540 2545 2550

gct ttc gcc aaa gat ggt att gct tgt tgc gga tta tta gct aag agt 8124
 Ala Phe Ala Lys Asp Gly Ile Ala Cys Cys Gly Leu Leu Ala Lys Ser
 2555 2560 2565

ttt aat gtt gaa gaa aga gat ata att aca gca tca tcc cac aag gca 8172
 Phe Asn Val Glu Glu Arg Asp Ile Ile Thr Ala Ser Ser His Lys Ala
 2570 2575 2580

gat ata aca ata ctt gac tgg gat atg caa agc gat agt ggg caa ttt	8220
Asp Ile Thr Ile Leu Asp Trp Asp Met Gln Ser Asp Ser Gly Gln Phe	
2585 2590 2595	
gct att gaa ata ata aaa tcg ata atc gtt tca gat ata aat tct gga	8268
Ala Ile Glu Ile Ile Lys Ser Ile Ile Val Ser Asp Ile Asn Ser Gly	
2600 2605 2610	
gga cgt tta cgt ctt ctt tct att tat act ggt gaa cat gtt act gct	8316
Gly Arg Leu Arg Leu Leu Ser Ile Tyr Thr Gly Glu His Val Thr Ala	
2615 2620 2625 2630	
gtt ata act aag ttg aac aat gag tta aag aaa aca tac cgt agc gta	8364
Val Ile Thr Lys Leu Asn Asn Glu Leu Lys Lys Thr Tyr Arg Ser Val	
2635 2640 2645	
ata aaa aat gat gat agt att ttt att gaa gat aac tat gca ctc gaa	8412
Ile Lys Asn Asp Asp Ser Ile Phe Ile Glu Asp Asn Tyr Ala Leu Glu	
2650 2655 2660	
caa tgg tgt ata gtt gtt att agt aaa gac gtt tat gaa aaa gat ctt	8460
Gln Trp Cys Ile Val Val Ile Ser Lys Asp Val Tyr Glu Lys Asp Leu	
2665 2670 2675	
cca aat gtg tta ata aaa aaa ttc act aac ctt aca gct ggg ttg cta	8508
Pro Asn Val Leu Ile Lys Lys Phe Thr Asn Leu Thr Ala Gly Leu Leu	
2680 2685 2690	
tcc aac gcc gca ctc tct tgc att tct gaa ata aga gaa aaa acc cat	8556
Ser Asn Ala Ala Leu Ser Cys Ile Ser Glu Ile Arg Glu Lys Thr His	
2695 2700 2705 2710	
ggg ata tta aca aaa tat aat aat aaa tta gac act gca tat gtt tcc	8604
Gly Ile Leu Thr Lys Tyr Asn Asn Lys Leu Asp Thr Ala Tyr Val Ser	
2715 2720 2725	
cac atc tta aat tta ata aaa tcc aag gag tca agg gca tat gct tat	8652
His Ile Leu Asn Leu Ile Lys Ser Lys Glu Ser Arg Ala Tyr Ala Tyr	
2730 2735 2740	
gaa aat gct cat gat tat gca gta gat tta att tct gaa gaa ata aga	8700
Glu Asn Ala His Asp Tyr Ala Val Asp Leu Ile Ser Glu Glu Ile Arg	
2745 2750 2755	
tca ata ttg caa ata agt gaa aac tta aag aaa tct cta agc aaa aac	8748
Ser Ile Leu Gln Ile Ser Glu Asn Leu Lys Lys Ser Leu Ser Lys Asn	
2760 2765 2770	

79

tta ctc gtt gaa aaa ata tct act cca aaa gta ttg aaa tgg atc ggg 9372
 Leu Leu Val Glu Lys Ile Ser Thr Pro Lys Val Leu Lys Trp Ile Gly
 2970 2975 2980

gaa ata aaa aca acg tac gcg caa aaa ata aca act gat att gtt gct 9420
 Glu Ile Lys Thr Thr Tyr Ala Gln Lys Ile Thr Thr Asp Ile Val Ala
 2985 2990 2995

aat ctg tca aga ata ggt tta gat caa cat gag tgg tta cga ata aaa 9468
 Asn Leu Ser Arg Ile Gly Leu Asp Gln His Glu Trp Leu Arg Ile Lys
 3000 3005 3010

tca aaa gat ata taaatgatta tatatgccgt cgttttataa aaactggcgg 9520
 Ser Lys Asp Ile
 3015

catgtatatac tagttagtcc atcatagaag tcaagaaatt tagtttgccc tatatcttat 9580

agaaaatata ttttatatgc ttaaaaaaca ccatctttct aagatggcat ttatgtgctt 9640

tgtttcgatc aattacaact gatataattac catattgatt aattttatgt tatttaccaa 9700

agtaacggca tcttaatatata tcgtcataat atagtgcgcg ttctgactct aatactgaaa 9760

aatttatttg ttctatttta cacttactgc aaatagcatc cagtttatca tatagtgtcg 9820

catcaattgg cgcag atg tca tca cgc caa atc ctt gag cat tat aat gct 9871
 Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala
 3020 3025 3030

cta aca tat ccc cta cat caa tca atc ttg ttg cag ata atg act tcg 9919
 Leu Thr Tyr Pro Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser
 3035 3040 3045

aat ttg tta tca gtt tgc act gga aaa tcc att tac gag gat atc tcc 9967
 Asn Leu Leu Ser Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser
 3050 3055 3060

ggc agt tct tgg aat atc ata cac ttc aat atc cct ctc ccc atc tct 10015
 Gly Ser Ser Trp Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser
 3065 3070 3075

aga gcg aga ctt tcc ata ttt tct tat tgt gtc aga att aaa cct tgg 10063
 Arg Ala Arg Leu Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp
 3080 3085 3090

atg agt atg gat tac atg taaccggctc atttaaaccg tctgggtctgt 10111
 Met Ser Met Asp Tyr Met

3095

3100

ttcctccggt tttaaaaaa ta atg tcc atc att ttt aat gga cac tat cgt 10163
 Met Ser Ile Ile Phe Asn Gly His Tyr Arg
 3105 3110

atg aaa cac cgg act tgg atc act gaa gct tta cgt ctt cac ttt gaa 10211
 Met Lys His Arg Thr Trp Ile Thr Glu Ala Leu Arg Leu His Phe Glu
 3115 3120 3125

gaa cat tta ccc cag gtt gtg gtc ggg cgt cgc ctg ggc gta cca aaa 10259
 Glu His Leu Pro Gln Val Val Val Gly Arg Arg Leu Gly Val Pro Lys
 3130 3135 3140

tca aca gct tgt ggt atg ttc gtg cgc ttt cgc aaa gct ggc ttt tca 10307
 Ser Thr Ala Cys Gly Met Phe Val Arg Phe Arg Lys Ala Gly Phe Ser
 3145 3150 3155

tgg cct ctg ccc gca ggt atg tcg gag cgg gag ctt gat ggc cgt ctt 10355
 Trp Pro Leu Pro Ala Gly Met Ser Glu Arg Glu Leu Asp Gly Arg Leu
 3160 3165 3170

tac ggg agt acc tcc aca gta cct gtc gta ctt tgt agt gga tcg gta 10403
 Tyr Gly Ser Thr Ser Thr Val Pro Val Val Leu Cys Ser Gly Ser Val
 3175 3180 3185 3190

att cag gac acc tcg aaa tcc tgt taatgttaaa acagtgaataa tgaggtgatg 10457
 Ile Gln Asp Thr Ser Lys Ser Cys
 3195

c atg atc aaa act cgt cgg act aaa cgt acc ttt tcc ccg gag ttc aag 10506
 Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys
 3200 3205 3210

ctt gaa gct ttc gag cag gtg gtg gtt aaa tac cag cgt gat gtc aga 10554
 Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg
 3215 3220 3225 3230

gaa gtc gcg cag gca ctc gag ctc aac cct gac cat ttg cgt aaa tgg 10602
 Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp
 3235 3240 3245

ata cgg ttg tat aag cag gaa ctt cag ggt att gag cca gct ggt aat 10650
 Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn
 3250 3255 3260

gct att acc cct gaa caa cgc gaa att cag cag ctt aaa gcg cag ata 10698
 Ala Ile Thr Pr Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile

3265

3270

3275

aag cgc gtt gag atg gaa aaa gaa ata cta aag cag gct gcc gtg ctg 10746
 Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu

3280

3285

3290

atg agc gaa atc ccc ggg aag ctg tcg cgc taatcacaca gctgaaagca 10796
 Met Ser Glu Ile Pro Gly Lys Leu Ser Arg

3295

3300

aagtggccag tgtgggttat ttgtcattta ttcggtatta accgtagcgt ttattacgcg 10856

caggtgaagc gtcctgttaa tgtgcaaaga attgaattac gaagccgggt gagggctttc 10916

catgctctca gtcgtggcgc agccgggtag ccgggcaatc agtcagatgt tgcgccagag 10976

tggcggttgat gcaggccgggt ggctggcatg acgactgatg cgggaatgag ggctgacaag 11036

tcgacagccg gttaaaccatc acaaccgggt aaacgaagac aaaagtccgc cattgccaaa 11096

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11165

<210> 35

<211> 366

<212> PRT

<213> Escherichia coli

<400> 35

Ser Asp Met Gln Arg Gly Ile Gln Ala Ala Thr Ala Ala Leu Gln Gly
 1 5 10 15

Leu Val Gly Gly Asn Met Ala Gly Ala Leu Ala Gly Ala Ser Ala Pro
 20 25 30

Glu Leu Ala Asn Ile Ile Gly His His Ala Gly Ile Asp Asp Asn Thr
 35 40 45

Ala Ala Lys Ala Ile Ala His Ala Ile Leu Gly Gly Val Thr Ala Ala
 50 55 60

Leu Gln Gly Asn Ser Ala Ala Ala Gly Ala Ile Gly Ala Gly Thr Gly
 65 70 75 80

Glu Val Ile Ala Ser Ala Ile Ala Lys Ser Leu Tyr Pr Gly Val Asp
 85 90 95

Pro Ser Lys Leu Thr Glu Asp Gln Lys Gln Thr Val Ser Thr Leu Ala
 100 105 110

Thr Leu Ser Ala Gly Met Ala Gly Gly Ile Ala Ser Gly Asp Val Ala
 115 120 125

Gly Ala Ala Ala Gly Ala Gly Ala Gly Lys Asn Val Val Glu Asn Asn
 130 135 140

Ala Leu Ser Leu Val Ala Arg Gly Cys Ala Val Ala Ala Pro Cys Arg
 145 150 155 160

Thr Lys Val Ala Glu Gln Leu Leu Glu Ile Gly Ala Lys Ala Gly Met
 165 170 175

Ala Gly Leu Ala Gly Ala Ala Val Lys Asp Met Ala Asp Arg Met Thr
 180 185 190

Ser Asp Glu Leu Glu His Leu Ile Thr Leu Gln Met Met Gly Asn Asp
 195 200 205

Glu Ile Thr Thr Lys Tyr Leu Ser Ser Leu His Asp Lys Tyr Gly Ser
 210 215 220

Gly Ala Ala Ser Asn Pro Asn Ile Gly Lys Asp Leu Thr Asp Ala Glu
 225 230 235 240

Lys Val Glu Leu Gly Gly Ser Gly Ser Gly Thr Gly Thr Pro Pro Pro
 245 250 255

Ser Glu Asn Asp Pro Lys Gln Gln Asn Glu Lys Thr Val Asp Lys Leu
 260 265 270

Asn Gln Lys Gln Glu Ser Ala Ile Lys Lys Ile Asp Asn Thr Ile Lys
 275 280 285

Asn Ala Leu Lys Asp His Asp Ile Ile Gly Thr Leu Lys Asp Met Asp
 290 295 300

Gly Lys Pro Val Pro Lys Glu Asn Gly Gly Tyr Trp Asp His Met Gln
 305 310 315 320

Glu Met Gln Asn Thr Leu Arg Gly Leu Arg Asn His Ala Asp Thr Leu
 325 330 335

Lys Asn Val Asn Asn Pro Glu Ala Gln Ala Ala Tyr Gly Arg Ala Thr
 340 345 350

Asp Ala Ile Asn Lys Ile Glu Ser Ala Leu Lys Gly Tyr Gly
 355 360 365

<210> 36

<211> 128

<212> PRT

<213> Escherichia coli

<400> 36

Met Ile Thr Leu Arg Lys Leu Ile Gly Asn Ile Asn Met Thr Lys Glu
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Pro Glu Gln Gln Ser Pro Leu Glu Leu Trp Phe Glu Arg Ile Ile Asp
 20 25 30

Val Pro Leu Glu Lys Leu Thr Val Glu Asp Leu Cys Arg Ala Ile Arg
 35 40 45

Gln Asn Leu Cys Ile Asp Gln Leu Met Pro Arg Val Leu Glu Val Leu
 50 55 60

Thr Lys Glu Pro Leu Ala Gly Glu Tyr Tyr Asp Gly Glu Leu Ile Ala
 65 70 75 80

Ala Leu Ser Thr Ile Lys Gly Glu Asp Leu Lys Asp Gln Lys Ser Thr
 85 90 95

Phe Thr Gln Ile Arg Gln Leu Ile Asn Gln Leu Glu Pro Ser Asp Ile
 100 105 110

Asn Asp Asp Leu Arg Lys Asp Ile Leu Lys Ile Asn Gln Ile Ile Val
 115 120 125

<210> 37

<211> 107

<212> PRT

<213> Escherichia coli

<400> 37

Met Val Ala Lys Ala Phe Ala Tyr Ala Leu Asn Gln Trp Pro Ala Leu
 1 5 10 15

Thr Tyr Tyr Ala Asn Asp Gly Trp Val Glu Ile Asp Asn Asn Ile Ala
 20 25 30

Glu Asn Ala Leu Arg Ala Val Ser Leu Gly Arg Lys Asn Phe Leu Phe
 35 40 45

Phe Gly Ser Asp His Gly Gly Glu Arg Gly Ala Leu Leu Tyr Ser Leu
 50 55 60

Ile Gly Thr Cys Lys Leu Asn Asp Val Asp Pro Glu Ser Tyr Leu Arg
 65 70 75 80

His Val Leu Ala Val Ile Ala Asp Trp Pro Val Asn Arg Val Ser Glu
 85 90 95

Leu Leu Pro Trp Arg Ile Ala Leu Pro Ala Glu
 100 105

<210> 38

<211> 86

<212> PRT

<213> Escherichia coli

<400> 38

Met Leu Met Ser Val Gln Lys Glu Lys Asn Val Ala Glu Ser Val Val
 1 5 10 15

Ser Glu Thr His Thr Gly Asp Ser Val Tyr Ala Ser Leu Phe Glu Lys
 20 25 30

Ile Asn Leu Asn Pro Val Ser Ala Leu Ser Ala Leu Asp Asn Pro Phe
 35 40 45

Arg Ser Ala Asp Asn Ala Thr Gly Arg Ile Thr Ser Ser Ile Gln Pro
 50 55 60

Ala Val Gln Cys Ala Ala Ala Ala Thr Glu Gly Ser Cys Pro Arg
 65 70 75 80

Gln Ser Pro Cys Ser Gly
 85

<210> 39

<211> 111

<212> PRT

<213> Escherichia coli

<400> 39

Met Val Asp Asn Trp Gln Lys Ser Val Arg Ser Arg Ala Leu Pro Glu

1 5 10 15
 Glu Ala Met Thr Gly Trp Asn Glu Gly Met Ile Arg Leu Gln Gln Leu
 20 25 30
 Ala Glu Arg Leu Asn Arg Gln Asp Glu Gln Arg Gly Lys Tyr Met Thr
 35 40 45
 Val Ser Glu Leu Lys Thr Glu Val Phe Gly Ile Met Gln Ala Phe Asn
 50 55 60
 Arg His Ile Pro Ala Glu Glu Gln Leu Arg Arg Tyr Gly Glu Val Arg
 65 70 75 80
 Asn Gln Asn Gly Ser Glu Gln Gln Gln Lys Gln Ala Glu Met Ala Leu
 85 90 95
 Asn Gln Leu Ile Asn Arg Tyr Gln Met Ile Arg Ala Gly Lys Gln
 100 105 110

 <210> 40
 <211> 143
 <212> PRT
 <213> Escherichia coli

 <400> 40
 Met Val Gly Cys Ala Trp Leu Ala Glu Gln Ala Phe Ser Asp His Ala
 1 5 10 15
 Leu Ser Pro His Ser Ala Trp Pro Tyr Ser Ala Ser Arg Asp Ala Gly
 20 25 30
 Leu Ala Asp Thr Gly Ala Gly Gly Tyr Pro Thr Cys Lys Gln Arg Trp
 35 40 45
 Ala Asp Asp Thr Val Gly Leu Lys Ala Arg Leu Leu Gln Leu Pro Ala
 50 55 60
 Leu Asp Ile Trp Thr Ala Phe Lys Lys Ile Asp Gln Ser Gln Val Val
 65 70 75 80
 Tyr Glu Glu Ala Val Leu Arg Ser Arg Val Ser Glu Arg Asn Met Gln
 85 90 95
 Val Ser Gln Asn Gly Arg Val Tyr Pro Ser Tyr Gly Gly Asn Val Asp
 100 105 110

Gly Thr Val Ala Asn Ala Ala Thr Arg Leu Ala Ser Gly Ala Arg Asn
 115 120 125

Ile Leu Gly Ser Ile Ala Ala Cys Thr Ala Phe Asp Ser Val Arg
 130 135 140

<210> 41

<211> 118

<212> PRT

<213> Escherichia coli

<400> 41

Met Val Gln Ala Gln Leu Gln Ile Ala Leu Val Ile Cys Ile Pro Leu
 1 5 10 15

Ile Thr Leu Cys Ser Ala Trp Asp Val Lys Val Val Met Thr Leu Thr
 20 25 30

Phe Val Gln Phe Ala Leu Phe Phe Leu Thr Phe Trp Trp Glu Leu Ala
 35 40 45

Arg Trp Leu Asp Ser Trp Leu Leu Asp Val Leu Tyr Asn Ser Asp Thr
 50 55 60

His Ser Ser Trp Asn Leu Ala Gly Ile Gln Asn Thr Gln Asp Asp Val
 65 70 75 80

Ile Ile Asn Leu Val Met Arg Leu Met Phe Leu Val Leu Pro Thr Phe
 85 90 95

Trp Leu Gly Ala Met Thr Trp Ala Gly Val Arg Val Gly Val Ala Leu
 100 105 110

Asn Gly Ala Leu Ala Gly
 115

<210> 42

<211> 81

<212> PRT

<213> Escherichia coli

<400> 42

Met Lys Tyr Leu Phe Phe Glu Asn Ile His Ser Ile Phe Leu Thr Phe
 1 5 10 15

Ser Leu Phe Arg Thr Ser Val Ser Pro Asp Phe Pro Met Ile Phe Ala

Ala

<400> 43
Leu Ile Val Ile Asp Phe Phe Cys Gly Cys Gly Gly Ala Ser Glu Gly
1 5 10 15

Leu Arg Gln Ala Gly Phe Asp Ile Glu Leu Gly Leu Asp Ile Asp Gln
20 25 30

Gln Ala Ser Glu Thr Phe Lys Ala Asn Phe Pro Asp Ala Lys Phe Ile
35 40 45

Gln Asp Asp Ile Arg Lys Ile Glu Pro Gln Asp Ile Ser Asp Ile Ile
50 55 60

Asp Ile Lys Ala Lys Arg Pro Leu Leu Leu Ser Ala Cys Ala Pro Cys
65 70 75 80

Gln Pro Phe Ser Gln Gln Asn Lys Asn Lys Thr Ser Asp Asp Ser Arg
85 90 95

Arg Asn Leu Leu Asn Glu Thr His Arg Phe Ile Arg Glu Leu Leu Pro
100 105 110

Glu Tyr Ile Met Leu Glu Asn Val Pro Gly Met Gln Lys Ile Asp Glu
115 120 125

Glu Lys Glu Gly Pro Phe Gln Glu Phe Ile Lys Leu Leu Lys Glu Leu
130 135 140

Glu Tyr Asn Tyr Ile Ser Phe Ile Ala Asn Ala Glu Asn Tyr Gly Ile

145	150	155	160
Pro Gln Arg Arg Lys Arg Leu Val Leu Leu Ala Ser Arg Val Gly Lys	165	170	175
Val Thr Leu Pro Glu Ile Thr His Gly Lys Asn Lys Ile Pro Phe Lys	180	185	190
Thr Val Arg Asp Tyr Ile Gln Asp Phe Thr Lys Leu Cys Ser Gly Glu	195	200	205
Thr Asp Pro Lys Asp Pro Leu His Arg Ala Gly Thr Leu Ser Pro Leu	210	215	220
Asn Leu Lys Arg Ile Met His Thr Pro Glu Gly Gly Asp Arg Arg Asn	225	230	235
Trp Pro Glu Glu Leu Val Asn Lys Cys His Lys Asn Tyr Asp Gly His	245	250	255
Thr Asp Thr Tyr Gly Arg Met Ser Trp Asp Lys Pro Ala Pro Thr Leu	260	265	270
Thr Thr Lys Cys Asn Ser Tyr Ser Asn Gly Arg Phe Gly His Pro Asp	275	280	285
Pro Thr Gln His Arg Ala Ile Ser Ile Arg Glu Ala Ser Arg Leu Gln	290	295	300
Thr Phe Pro Leu Ser Tyr Val Phe Lys Gly Ser Leu Asn Ser Met Ala	305	310	315
Lys Gln Ile Gly Asn Ala Val Pro Cys Glu Leu Ala Arg Leu Phe Gly	325	330	335
Leu His Leu Ile Glu Asn Cys Thr Asn Lys Asp Ser	340	345	

<210> 44

<211> 974

<212> PRT

<213> Escherichia coli

<400> 44

Met	Leu	Gly	Arg	Gln	Gln	Ile	Ala	Gly	Ile	Pro	Thr	Ala	Leu	Ser	Glu
1				5				10					15		

Leu Phe Lys Asn Ala His Asp Ala Tyr Ala Asp Asn Val Glu Val Asp
 20 25 30

Phe Phe Arg Lys Glu Asn Leu Leu Ile Leu Arg Asp Asp Gly Leu Gly
 35 40 45

Met Thr Thr Asp Glu Phe Glu Glu Arg Trp Leu Thr Ile Gly Thr Ser
 50 55 60

Ser Lys Leu Ile Asp Asp Asp Ala Ile Asn Lys Pro Ala Val Asp Ser
 65 70 75 80

Asn Lys Ala Phe Arg Pro Ile Met Gly Glu Lys Gly Ile Gly Arg Leu
 85 90 95

Ser Ile Ala Ala Ile Gly Pro Gln Val Leu Val Leu Thr Arg Ala Lys
 100 105 110

Arg Asp Asn Glu Leu Lys Pro Leu Val Ala Ala Phe Val Asn Trp Ser
 115 120 125

Leu Phe Ala Ile Pro Ser Leu Asp Leu Asp Asp Ile Glu Ile Pro Ile
 130 135 140

Arg Thr Ile Ile Asn Asp Glu Cys Phe Thr Lys Lys Thr Leu Asp Glu
 145 150 155 160

Met Ile Glu Gln Ala Arg Asn Asn Leu Asp Ser Leu Ser His Lys Ile
 165 170 175

Ser Lys Ser Lys Val Ser Gln Ile Asn Thr Gln Leu Ser Ser Phe Glu
 180 185 190

Phe Asp Pro Ile Leu Trp Glu Lys Lys Leu Gly Gly Leu Arg Leu Ser
 195 200 205

Gly Asp Gly His Gly Thr His Phe Ile Ile Met Pro Thr Glu Glu Ile
 210 215 220

Leu Ile Asp Asp Ile Ser Thr Ser Asp Ser Asn Lys Thr Ser Glu Gln
 225 230 235 240

Ser Ser Arg Leu Glu Lys Ala Leu Leu Gly Phe Thr Asn Thr Met Tyr
 245 250 255

Ser Asp Ser Asn Pr Pro Ile Ile Ala Arg Phe Arg Asp Tyr Leu Glu
 260 265 270

Asp Gly Glu Cys Ile Asp Arg Ile Ser Glu Ser Ile Phe Phe Thr Pro
 275 280 285
 Gln Glu Phe Asn Leu Ala Asp His His Ile Glu Gly Trp Phe Asn Glu
 290 295 300
 Phe Gly Gln Phe Ser Gly Thr Val Ser Val Tyr Gly Glu Glu Pro Ile
 305 310 315 320
 His His Val Val Thr Trp Lys Asn Asn Asn Gln Leu Thr Gln Cys Gly
 325 330 335
 Pro Phe Lys Ile Lys Leu Ala Tyr Ile His Gly Arg Leu Arg Asp Ser
 340 345 350
 Arg Leu Pro Met Glu Leu Trp Ala Pro Leu Lys Glu Lys Thr Asp Arg
 355 360 365
 Tyr Gly Gly Leu Tyr Ile Tyr Arg Asp Gly Leu Arg Ile Leu Pro Tyr
 370 375 380
 Gly Asp Ser Asp Thr Asp Phe Leu Lys Ile Glu Lys Arg Arg Thr Leu
 385 390 395 400
 Ser Ala Ser Glu Tyr Phe Phe Ser Tyr Arg Arg Leu Phe Gly Ala Ile
 405 410 415
 Glu Leu Thr Lys Glu Asn Asn Ala Ser Leu Val Glu Lys Ala Gly Arg
 420 425 430
 Glu Gly Phe Ile Glu Asn Lys Pro Tyr Lys Gln Phe Lys Glu Met Leu
 435 440 445
 Glu Asn Phe Phe Ile Glu Ile Ala Arg Asp Phe Phe Lys Asp Asp Gly
 450 455 460
 Asp Met Ser Glu Leu Phe Val Glu Thr Lys Gln Arg Arg Asn Glu Glu
 465 470 475 480
 His Asp Leu Leu Ser Lys Arg Ser Lys Gln Thr Lys Ala Lys Lys Asp
 485 490 495
 Arg Leu Lys Lys Asp Leu Tyr Asp Phe Phe Asp Lys Leu Asp Asn Asp
 500 505 510
 Tyr Trp Asn Ile Glu Ile Asn Lys Leu Ile Asn Lys Asn Glu Glu Tyr
 515 520 525

Phe Ser Ser Thr Glu Ile Thr Asp Thr Asn Ile Asp Tyr Val Tyr Asn
 530 535 540

Lys Ile Lys Glu Gln Asn Asp Ala Ile Ile Lys Asn Leu Arg Asn Ser
 545 550 555 560

Val Asp Ile Lys Lys Pro Ser Gly Val Gly Leu Thr Lys Glu Leu Ser
 565 570 575

Asn Leu Trp Asp Arg Tyr Gln Ile Glu Arg Gln Lys Ile Leu Leu Ser
 580 585 590

Leu Asn Glu Leu Lys Asp Asn Val Asp Arg Lys Leu Ile Glu Leu Asp
 595 600 605

Asn Lys Asn Asn Asp Phe Leu Asn Leu Arg Lys Arg Leu Glu Asp Ser
 610 615 620

Leu Asn Leu Gln Gln Ser Tyr Tyr Glu Lys Glu Leu Thr Lys Leu Tyr
 625 630 635 640

Asn Asp Ala Lys Asn Ala Leu Lys Asp Val Gln Ser Lys Ala Asn Arg
 645 650 655

Leu Ile Ser Asp Asn Lys Lys Lys His Lys Ser Glu Leu Lys Asn Ile
 660 665 670

Ser Tyr Glu Phe Gln Ser Thr Asn Leu Asn Gly Lys Asp Thr Ala Tyr
 675 680 685

Ile Leu Asp Val Lys Arg Asn Leu Glu Ser Lys Ile Glu Asn Thr Ser
 690 695 700

Asn Glu Val Ile Asn Glu Ile Arg Lys Leu Thr Asp Gln Ile Ala Ile
 705 710 715 720

Ile Ser Asp Ser Thr Thr Ser Glu Asn Leu Ser Ser Ala Gln Val Thr
 725 730 735

Glu Ala Ile Glu Thr Glu Leu Glu His Leu Arg Asp Gln Gln Ala Asn
 740 745 750

Asn Ala Glu Leu Ile Leu Leu Gly Met Ala Leu Ser Val Val His His
 755 760 765

Glu Phe Asn Gly Asn Ile Arg Ala Ile Arg Ser Ala Leu Arg Glu Leu
 770 775 780

Lys Ala Trp Ala Asp Arg Asn Pro Lys Leu Asp Ile Ile Tyr Gln Lys
785 790 795 800

Ile Arg Thr Ser Phe Asp His Leu Asp Gly Tyr Leu Lys Thr Phe Thr
805 810 815

Pro Leu Thr Arg Arg Leu Ser Arg Ser Lys Thr Asn Ile Thr Gly Thr
820 825 830

Ala Ile Leu Glu Phe Ile Arg Asp Val Phe Asp Asp Arg Leu Glu Lys
835 840 845

Glu Gly Ile Glu Leu Phe Thr Thr Ser Lys Phe Val Asn Gln Glu Ile
850 855 860

Val Thr Tyr Thr Ser Thr Ile Tyr Pro Val Phe Ile Asn Leu Ile Asp
865 870 875 880

Asn Ala Ile Tyr Trp Leu Gly Lys Thr Thr Gly Glu Lys Arg Leu Ile
885 890 895

Leu Asp Ala Thr Glu Thr Gly Phe Val Ile Gly Asp Thr Gly Pro Gly
900 905 910

Val Ser Thr Arg Asp Arg Asp Ile Ile Phe Asp Met Gly Phe Thr Arg
915 920 925

Lys Thr Gly Gly Arg Gly Met Gly Leu Phe Ile Ser Lys Glu Cys Leu
930 935 940

Ser Arg Asp Gly Phe Thr Ile Arg Leu Asp Asp Tyr Thr Pro Glu Gln
945 950 955 960

Gly Ala Phe Phe Ile Ile Glu Pro Ser Glu Glu Thr Ser Glu
965 970

<210> 45

<211> 555

<212> PRT

<213> Escherichia coli

<400> 45

Met Thr Ser Ser Thr Asp Phe His Lys Leu Ser Glu Asp Cys Val Arg
1 5 10 15

Arg Phe Leu His Ser Val Val Ala Val Asp Asp Asn Met Ser Phe Gly
20 25 30

Ala Gly Ser Asp Thr Phe Pro Thr Asp Glu Asp Ile Asn Ala Leu Val
 35 40 45
 Asp Pro Asp Asp Asp Pro Thr Pro Ile Ile Thr Ala Ser Ala Ser Pro
 50 55 60
 Arg Ile Glu Ser Thr Lys Ser Lys Ala Lys Val Lys Asn His Pro Phe
 65 70 75 80
 Asp Tyr Gln Ala Leu Ala Glu Ala Phe Ala Lys Asp Gly Ile Ala Cys
 85 90 95
 Cys Gly Leu Leu Ala Lys Ser Phe Asn Val Glu Glu Arg Asp Ile Ile
 100 105 110
 Thr Ala Ser Ser His Lys Ala Asp Ile Thr Ile Leu Asp Trp Asp Met
 115 120 125
 Gln Ser Asp Ser Gly Gln Phe Ala Ile Glu Ile Ile Lys Ser Ile Ile
 130 135 140
 Val Ser Asp Ile Asn Ser Gly Gly Arg Leu Arg Leu Leu Ser Ile Tyr
 145 150 155 160
 Thr Gly Glu His Val Thr Ala Val Ile Thr Lys Leu Asn Asn Glu Leu
 165 170 175
 Lys Lys Thr Tyr Arg Ser Val Ile Lys Asn Asp Asp Ser Ile Phe Ile
 180 185 190
 Glu Asp Asn Tyr Ala Leu Glu Gln Trp Cys Ile Val Val Ile Ser Lys
 195 200 205
 Asp Val Tyr Glu Lys Asp Leu Pro Asn Val Leu Ile Lys Lys Phe Thr
 210 215 220
 Asn Leu Thr Ala Gly Leu Leu Ser Asn Ala Ala Leu Ser Cys Ile Ser
 225 230 235 240
 Glu Ile Arg Glu Lys Thr His Gly Ile Leu Thr Lys Tyr Asn Asn Lys
 245 250 255
 Leu Asp Thr Ala Tyr Val Ser His Ile Leu Asn Leu Ile Lys Ser Lys
 260 265 270
 Glu Ser Arg Ala Tyr Ala Tyr Glu Asn Ala His Asp Tyr Ala Val Asp
 275 280 285

Leu Ile Ser Glu Glu Ile Arg Ser Ile Leu Gln Ile Ser Glu Asn Leu
 290 295 300

Lys Lys Ser Leu Ser Lys Asn Ser Leu Ser His Trp Pro Ile Phe His
 305 310 315 320

Tyr Ala Lys Asn Gly Cys Lys Asn Phe Leu Leu Thr Gly Lys Lys Gln
 325 330 335

Lys Asp Leu Ser Val Glu His Leu Arg Asn Ile Leu Ser Ala Asp Ser
 340 345 350

Leu Glu Glu Ile Gln His Ala Ile Glu His Ala Ser Leu Gly Lys Lys
 355 360 365

Glu Tyr Leu Ser Gln Asp Gly Glu Glu Asp Lys Lys Leu Met Gln Leu
 370 375 380

Cys Ser Leu Glu Ile Thr Arg Arg Ser Leu Arg Tyr His Ser His Ile
 385 390 395 400

Asp Asn Val Ser Leu Lys Gln Gly Thr Leu Leu Leu Asp Ala Tyr Asn
 405 410 415

Phe Val Tyr Leu Cys Ile Gln Pro Leu Cys Asp Ser Val Arg Leu His
 420 425 430

Glu Lys Ala Asp Phe Leu Phe Leu Arg Gly Thr Leu Asp Asp Asn Asn
 435 440 445

Tyr Asn Leu Leu Ile Glu Asp Glu Tyr Gly Gly Phe Tyr Lys Ile Lys
 450 455 460

Met Pro Ala Lys Ala Ser Asn Ile Ile Ser Phe Ser Phe Gly Val Glu
 465 470 475 480

Asn Gly Asn Gly Val Ile Ile Gly Lys Lys Asn Asn Leu Val Asn Thr
 485 490 495

Asp Tyr Ile Ser Phe Val Pro Leu Leu Val Glu Lys Ile Ser Thr Pro
 500 505 510

Lys Val Leu Lys Trp Ile Gly Glu Ile Lys Thr Thr Tyr Ala Gln Lys
 515 520 525

Ile Thr Thr Asp Ile Val Ala Asn Leu Ser Arg Ile Gly Leu Asp Gln
 530 535 540

His Glu Trp Leu Arg Ile Lys Ser Lys Asp Ile
545 550 555

<210> 46

<211> 82

<212> PRT

<213> Escherichia coli

<400> 46

Met Ser Ser Arg Gln Ile Leu Glu His Tyr Asn Ala Leu Thr Tyr Pro
1 5 10 15

Leu His Gln Ser Ile Leu Leu Gln Ile Met Thr Ser Asn Leu Leu Ser
20 25 30

Val Cys Thr Gly Lys Ser Ile Tyr Glu Asp Ile Ser Gly Ser Ser Trp
35 40 45

Asn Ile Ile His Phe Asn Ile Pro Leu Pro Ile Ser Arg Ala Arg Leu
50 55 60

Ser Ile Phe Ser Tyr Cys Val Arg Ile Lys Pro Trp Met Ser Met Asp
65 70 75 80

Tyr Met

<210> 47

<211> 98

<212> PRT

<213> Escherichia coli

<400> 47

Met Ser Ile Ile Phe Asn Gly His Tyr Arg Met Lys His Arg Thr Trp
1 5 10 15

Ile Thr Glu Ala Leu Arg Leu His Phe Glu Glu His Leu Pro Gln Val
20 25 30

Val Val Gly Arg Arg Leu Gly Val Pro Lys Ser Thr Ala Cys Gly Met
35 40 45

Phe Val Arg Phe Arg Lys Ala Gly Phe Ser Trp Pro Leu Pro Ala Gly
50 55 60

Met Ser Glu Arg Glu Leu Asp Gly Arg Leu Tyr Gly Ser Thr Ser Thr

65	70	75	80
Val Pro Val Val Leu Cys Ser Gly Ser Val Ile Gln Asp Thr Ser Lys			
85	90	95	

Ser Cys

<210> 48

<211> 106

<212> PRT

<213> Escherichia coli

<400> 48

Met Ile Lys Thr Arg Arg Thr Lys Arg Thr Phe Ser Pro Glu Phe Lys
1 5 10 15

Leu Glu Ala Phe Glu Gln Val Val Val Lys Tyr Gln Arg Asp Val Arg
20 25 30

Glu Val Ala Gln Ala Leu Glu Leu Asn Pro Asp His Leu Arg Lys Trp
35 40 45

Ile Arg Leu Tyr Lys Gln Glu Leu Gln Gly Ile Glu Pro Ala Gly Asn
50 55 60

Ala Ile Thr Pro Glu Gln Arg Glu Ile Gln Gln Leu Lys Ala Gln Ile
65 70 75 80

Lys Arg Val Glu Met Glu Lys Glu Ile Leu Lys Gln Ala Ala Val Leu
85 90 95

Met Ser Glu Ile Pro Gly Lys Leu Ser Arg
100 105

<210> 49

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 49

tgctctagag ccattactca gaatggg

27

<210> 50

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 50

cgcgagctcg acgactgaat gatccc

26

<210> 51

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 51

tcccccggtt actgcagcac tcaacc

26

<210> 52

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 52

gatccccgga ccactgaaat gcgtgc

26

<210> 53

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 53

tcgtctagag atgatggtga tggagcg

27

<210> 54

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 54

gaactgcagc caaataactga taccaccc

28

<210> 55

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 55

gaactgcagg ctaaaacaga agacgcg

27

<210> 56

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 56

catgcatgca ctccatatga caaccgc

27

<210> 57

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 57

tcgtctagaa tgaagctgcg catgagg

27

<210> 58

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 58

caactgcagt cgcaaattgc gaactgg

27

<210> 59

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 59

caactgcaga ccgcaacttt tcgacgc

27

<210> 60

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 60

catgcatgcc agtgagccat tgttccc

27

<210> 61

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 61

tgctctagat acgactctga caggagg

27

<210> 62

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 62

tcagatatca actaccagca gtttgg

26

<210> 63

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 63

tcagatatcc ataaagagtg acgtggc

27

<210> 64

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 64

tgctctagaa aacgtggcaa cagagcg

27

<210> 65

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:Oligonucleotide

<400> 65

tgctctagaa ggcgttgctg atcctg

26

<210> 66
<211> 28
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 66
gaactgcagg aaaaggccga gcagactg 28

<210> 67
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 67
gaactgcagt acagccatgt ttacggt 27

<210> 68
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 68
catgcatgcg gtgtacgaca gtttgcg 27

<210> 69
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 69
tgctctagac acatcatggg cacacc 26

<210> 70
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 70
gaactgcaga accgtccaca tcaggcg 27

<210> 71
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 71
gaactgcaga ccctgcttgc cattccg 27

<210> 72
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:Oligonucleotide

<400> 72
catgcatgca taagcgtcga acaggcg 27